

# UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 CFR 1.53(b))

Attorney Docket No.

GI 6069-74A

Total Pages

424

First Named Inventor or Application Identifier

Kenneth Jacobs et al.

## APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents.

ADDRESS TO: Assistant Commissioner for Patents  
Box Patent Application  
Washington, DC 20231

1. ☒ Fee Transmittal Form  
(Submit an original, and a duplicate for fee processing)

6. ☐ Microfiche Computer Program (Appendix)

2. ☒ Specification [Total Pages 295]  
(preferred arrangement set forth below)

7. Nucleotide and/or Amino Acid Sequence Submission  
(If applicable, all necessary)

- Descriptive title of the invention
- Cross References to Related Applications
- Statement Regarding Fed sponsored R & D
- Reference to Microfiche Appendix
- Background of the Invention
- Brief Summary of the Invention
- Brief Description of the Drawings (if filed)
- Detailed Description
- Claim(s)
- Abstract of the Disclosure

a. ☒ Computer Readable Copy

b. ☒ Paper Copy (identical to computer copy) (127pp.)

c. ☒ Statement verifying identity of above copies

3. ☒ Drawing(s) (35 USC 113) [Total Sheets 2]

4. Oath or Declaration [Total Pages ]

a. ☐ Unsigned (original or copy)

b. ☐ Copy from a prior application (37 CFR 1.63(d))  
(for continuation/divisional with Box 17 completed)

[Note Box 5 below]

i. ☐ DELETION OF INVENTOR(S)  
Signed statement attached deleting  
inventor(s) named in the prior application,  
See 37 CFR 1.63(d)(2) and 1.33(b).

5. ☐ Incorporation By Reference (useable if Box 4b is checked)  
The entire disclosure of the prior application, from which  
a copy of the oath or declaration is supplied under Box  
4b, is considered as being part of the disclosure of the  
accompanying application and is hereby incorporated by  
reference therein.

## ACCOMPANYING APPLICATION PARTS

8. ☐ Assignment Papers (cover sheet & documents(s))

9. ☐ 37 CFR 3.73(b) Statement ☐ Power of Attorney  
(when there is an assignee)

10. ☐ English Translation Document (if applicable)

11. ☐ Information Disclosure  
Statement (IDS)/PTO-1449 ☐ Copies of IDS  
Citations

12. ☐ Preliminary Amendment

13. ☒ Return Receipt Postcard (MPEP 503)  
(Should be specifically itemized)

14. ☐ Small Entity ☐ Statement filed in prior application,  
Statement(s) Status still proper and desired

15. ☐ Certified Copy of Priority Document(s)  
(if foreign priority is claimed)

16. ☒ Other: . . . Information Data Sheet. . . . .

17. If a **CONTINUING APPLICATION**, check appropriate box and supply the requisite information: 60/084,564, 60/087,645, 60/093,712  
☐ Continuation ☐ Divisional ☒ Continuation-in-part (CIP) of prior application No.: 60/094,935, 60/095,880, 60/096,068

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## CERTIFICATE OF EXPRESS MAILING

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Date May 6, 1999

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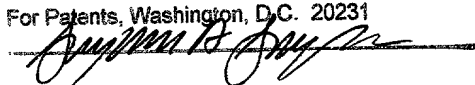
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#### Application Information

Title Line One ::  
 Title Line Two ::  
 Total Drawing Sheets ::  
 Formal Drawings ::  
 Application Type ::  
 Docket Number ::  
 Licensed - U S Government Agency ::  
 Contract Number ::  
 Grant Number ::  
 Secrecy Order in Parent Application ::

SECRETED PROTEINS AND  
 POLYNUCLEOTIDES ENCODING THEM  
 2  
 N  
 Utility  
 GI 6069-74A

## Representative Information

Representative Customer Number ::  
Registration Number One :: 41,323  
Registration Number Two :: 32,618  
Registration Number Three :: 32,245  
Registration Number Four :: 32,724

## Continuity Information

This application is a :: Continuation-in-Part of  
> Application One :: 60/084,564  
Filing Date :: May 7, 1998  
Patent Number ::  
This application is a :: Continuation-in-Part of  
> Application Two :: 60/087,645  
Filing Date :: June 2, 1998  
Patent Number ::  
This application is a :: Continuation-in-Part of  
> Application Three :: 60/093,712  
Filing Date :: July 22, 1998  
Patent Number ::  
This application is a :: Continuation-in-Part of  
> Application Four :: 60/094,935  
Filing Date :: July 31, 1998  
Patent Number ::  
This application is a :: Continuation-in-Part of  
> Application Five :: 60/095,880  
Filing Date :: August 10, 1998  
Patent Number ::  
This application is a :: Continuation-in-Part of  
> Application One :: 60/096,068  
Filing Date :: August 11, 1998  
Patent Number ::

## Prior Foreign Applications

Foreign Application One ::  
Filing Date ::  
Country ::  
Priority Claimed ::

SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

- 5 This application is a continuation-in-part of the following applications:
- (1) provisional application Ser. No. 60/084,564, filed May 7, 1998;
  - (2) provisional application Ser. No. 60/087,645, filed June 2, 1998;
  - (3) provisional application Ser. No. 60/093,712, filed July 22, 1998;
  - (4) provisional application Ser. No. 60/094,935, filed July 31, 1998;
  - 10 (5) provisional application Ser. No. 60/095,880, filed August 10, 1998;
  - (6) provisional application Ser. No. 60/096,068, filed August 11, 1998;
- all of which are incorporated by reference herein.

FIELD OF THE INVENTION

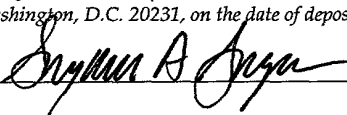
- 15 The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

BACKGROUND OF THE INVENTION

- 20 Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein
- 25 in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of
- 30 DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

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## SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bn365\_53 deposited under accession  
10 number ATCC 98752;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bn365\_53 deposited under accession number ATCC 98752;
- (e) a polynucleotide comprising the nucleotide sequence of a mature  
15 protein coding sequence of clone bn365\_53 deposited under accession number ATCC 98752;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bn365\_53 deposited under accession number ATCC 98752;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
- 20 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 25 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:1.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366; the nucleotide sequence of the full-length protein coding sequence of clone bn365\_53 deposited under accession number ATCC

98752; or the nucleotide sequence of a mature protein coding sequence of clone bn365\_53 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bn365\_53 deposited under accession number ATCC 98752. In further preferred  
5 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having  
10 biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:2.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1.

Further embodiments of the invention provide isolated polynucleotides produced  
15 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (aa) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

(ab) the nucleotide sequence of the cDNA insert of clone bn365\_53 deposited under accession number ATCC 98752;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

(bb) the nucleotide sequence of the cDNA insert of clone

bn365\_53 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to  
10 a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of  
15 SEQ ID NO:1 from nucleotide 61 to nucleotide 366, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
20 consisting of:

(a) the amino acid sequence of SEQ ID NO:2;

(b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and

(c) the amino acid sequence encoded by the cDNA insert of clone  
25 bn365\_53 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably  
30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bo342\_2 deposited under accession number ATCC 98752;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752;
- (f) a polynucleotide comprising the nucleotide sequence of a mature  
15 protein coding sequence of clone bo342\_2 deposited under accession number ATCC 98752;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752;
- (h) a polynucleotide encoding a protein comprising the amino acid  
20 sequence of SEQ ID NO:4;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:3.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915; the nucleotide sequence of SEQ ID NO:3



from nucleotide 1358 to nucleotide 1915; the nucleotide sequence of the full-length protein coding sequence of clone bo342\_2 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone bo342\_2 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 280 to amino acid 289 of SEQ ID NO:4.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:3.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(ab) the nucleotide sequence of the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(bb) the nucleotide sequence of the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:3 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the

15 cDNA sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915. Also preferably the polynucleotide isolated according to the above

20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:4;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and

(c) the amino acid sequence encoded by the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:4. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 280 to amino acid 289 of SEQ ID NO:4.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689;
- 15 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dn721\_8 deposited under accession number ATCC 98752;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dn721\_8 deposited under accession number ATCC 98752;
- 20 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- 25 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 30 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:5.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689; the nucleotide sequence of the full-length protein coding sequence of clone dn721\_8 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone dn721\_8 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 318 to amino acid 327 of SEQ ID NO:6.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:5.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

(ab) the nucleotide sequence of the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

(bb) the nucleotide sequence of the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5, and extending  
15 contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:5 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689, and extending  
20 contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689.

In other embodiments, the present invention provides a composition comprising  
25 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:6;

(b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:6. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 318 to amino acid 327 of SEQ ID NO:6.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dn834\_1 deposited under accession number ATCC 98752;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dn834\_1 deposited under accession number ATCC 98752;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:7.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484; the nucleotide sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892; the nucleotide sequence of the full-length protein coding sequence of clone dn834\_1 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone dn834\_1 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 72 to amino acid 81 of SEQ ID NO:8.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:7.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

(ab) the nucleotide sequence of the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and
    - (bb) the nucleotide sequence of the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752;
  - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:7 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;



(b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and

(c) the amino acid sequence encoded by the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:8, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 72 to amino acid 81 of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pd278\_5 deposited under accession number ATCC 98752;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pd278\_5 deposited under accession number ATCC 98752;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:9.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420; the nucleotide sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420; the nucleotide sequence of the full-length protein coding sequence of clone pd278\_5 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pd278\_5 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 98 to amino acid 107 of SEQ ID NO:10.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:9.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(ab) the nucleotide sequence of the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(bb) the nucleotide sequence of the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:9 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 803 to

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nucleotide 1420. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:10;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:10. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:10, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 98 to amino acid 107 of SEQ ID NO:10.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pe80\_1 deposited under accession number
- 30 ATCC 98752;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pe80\_1 deposited under accession number ATCC 98752;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:11.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295; the nucleotide sequence of the full-length protein coding sequence of clone pe80\_1 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pe80\_1 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:12.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:11.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(ab) the nucleotide sequence of the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

25 (bb) the nucleotide sequence of the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:11 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295, to a nucleotide  
5 sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:12;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:12. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
20 of SEQ ID NO:12, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:12.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
30 NO:13 from nucleotide 348 to nucleotide 428;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm113\_1 deposited under accession number ATCC 98752;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm113\_1 deposited under accession number ATCC 98752;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:13.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428; the nucleotide sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428; the nucleotide sequence of the full-length protein coding sequence of clone pm113\_1 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pm113\_1 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having



biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:14.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:13.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

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(aa) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and

(ab) the nucleotide sequence of the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752;

15

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25

(ba) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and

(bb) the nucleotide sequence of the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

5 ID NO:13 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:13 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:13. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
- (b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
- 20 (c) the amino acid sequence encoded by the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:14. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:14.

30 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;



comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 226 to amino acid 235 of SEQ ID NO:16.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and

- (ab) the nucleotide sequence of the cDNA insert of clone pm749\_8 deposited under accession number ATCC 98752;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and

- (bb) the nucleotide sequence of the cDNA insert of clone pm749\_8 deposited under accession number ATCC 98752;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:15 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:16;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pm749\_8 deposited under accession number ATCC 98752;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 226 to amino acid 235 of SEQ ID NO:16.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 2023;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 2023;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pt31\_4 deposited under accession number ATCC 98752;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pt31\_4 deposited under accession number ATCC 98752;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:17.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 2023; the nucleotide sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 2023; the nucleotide sequence of the full-length protein coding sequence of clone pt31\_4 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pt31\_4 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752. In further preferred embodiments, the

present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a polynucleotide encoding a protein comprising a  
5 fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 325 to amino acid 334 of SEQ ID NO:18.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:17.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
15 consisting of:

(aa) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

(ab) the nucleotide sequence of the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

(bb) the nucleotide sequence of the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:17 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide  
10 2023, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 2023, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 2023. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
15 NO:17 from nucleotide 137 to nucleotide 2023, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 2023, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 2023.

In other embodiments, the present invention provides a composition comprising  
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:18;
- (b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:18. In further preferred  
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 325 to amino acid 334 of SEQ ID NO:18.



In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pv296\_5 deposited under accession number ATCC 98752;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pv296\_5 deposited under accession number ATCC 98752;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least
- 30 25% of the length of SEQ ID NO:19.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299; the nucleotide sequence of the full-length protein coding sequence of clone pv296\_5 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pv296\_5

deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein  
5 comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 41  
10 to amino acid 50 of SEQ ID NO:20.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:19.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 20 (aa) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and
    - (ab) the nucleotide sequence of the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that  
30 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

- (bb) the nucleotide sequence of the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:19 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:20;
- (b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:20. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 41 to amino acid 50 of SEQ ID NO:20.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone er311\_20 deposited under accession number ATCC 98781;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone er311\_20 deposited under accession number ATCC 98781;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least
- 30 25% of the length of SEQ ID NO:21.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008; the nucleotide sequence of the full-length protein coding sequence of clone er311\_20 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone er311\_20

deposited under accession number ATCC 98781. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 328 to amino acid 337 of SEQ ID NO:22.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:21.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and
    - (ab) the nucleotide sequence of the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

(bb) the nucleotide sequence of the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ  
10 ID NO:21 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
15 of said sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
20 consisting of:

(a) the amino acid sequence of SEQ ID NO:22;

(b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and

(c) the amino acid sequence encoded by the cDNA insert of clone  
25 er311\_20 deposited under accession number ATCC 98781;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:22. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably  
30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 328 to amino acid 337 of SEQ ID NO:22.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fh149\_12 deposited under accession number ATCC 98781;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fh149\_12 deposited under accession number ATCC 98781;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:24;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:23.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043; the nucleotide sequence of SEQ ID NO:23

from nucleotide 919 to nucleotide 2043; the nucleotide sequence of the full-length protein coding sequence of clone fh149\_12 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone fh149\_12 deposited under accession number ATCC 98781. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 255 to amino acid 264 of SEQ ID NO:24.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:23.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(ab) the nucleotide sequence of the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:



(ba) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(bb) the nucleotide sequence of the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:23 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
15 corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043. Also preferably the polynucleotide isolated according to the above  
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:24;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and

(c) the amino acid sequence encoded by the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:24. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 255 to amino acid 264 of SEQ ID NO:24.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pc201\_6 deposited under accession number ATCC 98781;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pc201\_6 deposited under accession number ATCC 98781;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:26;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:25.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099; the nucleotide sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099; the nucleotide sequence of the full-length protein coding sequence of clone pc201\_6 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone pc201\_6 deposited under accession number ATCC 98781. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 170 to amino acid 179 of SEQ ID NO:26.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:25.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and

(ab) the nucleotide sequence of the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and

10 (bb) the nucleotide sequence of the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:25 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:25, but  
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:25. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099, to a nucleotide  
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from  
30 nucleotide 143 to nucleotide 1099, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:26;
- (b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:26. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably

10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 170 to amino acid 179 of SEQ ID NO:26.

In one embodiment, the present invention provides a composition comprising an

15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259;
- 20 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pl87\_1 deposited under accession number ATCC 98781;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pl87\_1 deposited under accession number ATCC 98781;
- 25 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pl87\_1 deposited under accession number ATCC 98781;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pl87\_1 deposited under accession number ATCC 98781;
- 30 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:27.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259; the nucleotide sequence of the full-length protein coding sequence of clone pl87\_1 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone pl87\_1 deposited under accession number ATCC 98781. In other preferred embodiments, the  
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pl87\_1 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most  
20 preferably thirty) contiguous amino acids of SEQ ID NO:28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:28.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
25 ID NO:27.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize  
30 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(ab) the nucleotide sequence of the cDNA insert of clone  
pl87\_1 deposited under accession number ATCC 98781;

(ii) hybridizing said probe(s) to human genomic DNA in  
conditions at least as stringent as 4X SSC at 50 degrees C; and

5 (iii) isolating the DNA polynucleotides detected with the  
probe(s);

and

(b) a process comprising the steps of:

10 (i) preparing one or more polynucleotide primers that  
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from  
the group consisting of:

(ba) SEQ ID NO:27, but excluding the poly(A) tail at the  
3' end of SEQ ID NO:27; and

15 (bb) the nucleotide sequence of the cDNA insert of clone  
pl87\_1 deposited under accession number ATCC 98781;

(ii) hybridizing said primer(s) to human genomic DNA in  
conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

20 Preferably the polynucleotide isolated according to the above process comprises a  
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27, and  
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ  
ID NO:27 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:27 , but  
excluding the poly(A) tail at the 3' end of SEQ ID NO:27. Also preferably the  
25 polynucleotide isolated according to the above process comprises a nucleotide sequence  
corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide  
259, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
of said sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259, to a nucleotide  
sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide  
30 5 to nucleotide 259.

In other embodiments, the present invention provides a composition comprising  
a protein, wherein said protein comprises an amino acid sequence selected from the group  
consisting of:

(a) the amino acid sequence of SEQ ID NO:28;

(b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and

(c) the amino acid sequence encoded by the cDNA insert of clone pl87\_1 deposited under accession number ATCC 98781;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:28, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:28.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284;

20 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm514\_4 deposited under accession number ATCC 98781;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781;

25 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm514\_4 deposited under accession number ATCC 98781;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781;

30 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;



(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:29.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284; the nucleotide sequence of the full-length protein coding sequence of clone pm514\_4 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone pm514\_4 deposited under accession number ATCC 98781. In other preferred embodiments, the  
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most  
20 preferably thirty) contiguous amino acids of SEQ ID NO:30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 365 to amino acid 374 of SEQ ID NO:30.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
25 ID NO:29.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and

(ab) the nucleotide sequence of the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and

(bb) the nucleotide sequence of the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:30;

(b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and

(c) the amino acid sequence encoded by the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:30. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:30, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 365 to amino acid 374 of SEQ ID NO:30.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone co155\_12 deposited under accession number ATCC 98808;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone co155\_12 deposited under accession number ATCC 98808;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:32;

- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:31.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997; the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997; the nucleotide sequence of the full-length protein coding sequence of clone co155\_12 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone co155\_12 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 322 to amino acid 331 of SEQ ID NO:32.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:31.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(ab) the nucleotide sequence of the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(bb) the nucleotide sequence of the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:31 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide

36 to nucleotide 1997. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:32;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:32. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:32, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 322 to amino acid 331 of SEQ ID NO:32.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 30 NO:33 from nucleotide 84 to nucleotide 1343;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fn189\_13 deposited under accession number ATCC 98808;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fn189\_13 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:34;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:33.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343; the nucleotide sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343; the nucleotide sequence of the full-length protein coding sequence of clone fn189\_13 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone fn189\_13 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having

biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:34.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:33.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(ab) the nucleotide sequence of the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(bb) the nucleotide sequence of the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ



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ID NO:33 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:33 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:33. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:34;
- (b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and
- (c) the amino acid sequence encoded by the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:34. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:34.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;



encodes the full-length or a mature protein encoded by the cDNA insert of clone lv2\_47 deposited under accession number ATCC 98808. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36 from amino acid 58 to amino acid 164. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 77 to amino acid 86 of SEQ ID NO:36.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:35.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

- (ab) the nucleotide sequence of the cDNA insert of clone lv2\_47 deposited under accession number ATCC 98808;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

(bb) the nucleotide sequence of the cDNA insert of clone lv2\_47 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:35 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide 557, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide 557, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide 557. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 235 to nucleotide 899, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 235 to nucleotide 899, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 235 to nucleotide 899.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:36;

(b) the amino acid sequence of SEQ ID NO:36 from amino acid 58 to amino acid 164;

(c) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and

(d) the amino acid sequence encoded by the cDNA insert of clone lv2\_47 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:36 or the amino acid sequence

of SEQ ID NO:36 from amino acid 58 to amino acid 164. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 77 to amino acid 86 of SEQ ID NO:36.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 215 to nucleotide 499;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ml243\_1 deposited under accession number ATCC 98808;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ml243\_1 deposited under accession number ATCC 98808;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:38;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:37.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499; the nucleotide sequence of SEQ ID NO:37 from nucleotide 215 to nucleotide 499; the nucleotide sequence of the full-length protein coding sequence of clone ml243\_1 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone ml243\_1 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:38.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:37.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(ab) the nucleotide sequence of the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

10 (bb) the nucleotide sequence of the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:37 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:37, but  
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:37. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499, to a nucleotide  
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 215 to nucleotide 499, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from  
30 nucleotide 215 to nucleotide 499, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 215 to nucleotide 499.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:38;
- (b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:38. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably  
 10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:38.

In one embodiment, the present invention provides a composition comprising an  
 15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861;
- 20 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm96\_9 deposited under accession number ATCC 98808;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808;
- 25 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm96\_9 deposited under accession number ATCC 98808;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808;
- 30 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;



(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:39.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861; the nucleotide sequence of the full-length protein coding sequence of clone pm96\_9 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone pm96\_9 deposited under accession number ATCC 98808. In other preferred embodiments, the  
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most  
20 preferably thirty) contiguous amino acids of SEQ ID NO:40, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 110 to amino acid 119 of SEQ ID NO:40.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
25 ID NO:39.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize  
30 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

- (ab) the nucleotide sequence of the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that
    - 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (ba) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and
      - (bb) the nucleotide sequence of the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808;
      - 15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
      - (iii) amplifying human DNA sequences; and
      - (iv) isolating the polynucleotide products of step (b)(iii).
  - 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:39 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39. Also preferably the
  - 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide
  - 30 2172 to nucleotide 2861.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;

(b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and

(c) the amino acid sequence encoded by the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:40. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:40, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 110 to amino acid 119 of SEQ ID NO:40.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pu261\_1 deposited under accession number ATCC 98808;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pu261\_1 deposited under accession number ATCC 98808;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:41.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762; the nucleotide sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762; the nucleotide sequence of the full-length protein coding sequence of clone pu261\_1 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone pu261\_1 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:42.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:41.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(ab) the nucleotide sequence of the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(bb) the nucleotide sequence of the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:41 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide

43 to nucleotide 762. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:42;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:42. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:42, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:42.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pw214\_15 deposited under accession number ATCC 98808;
- 30 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pw214\_15 deposited under accession number ATCC 98808;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:44;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:43.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824; the nucleotide sequence of the full-length protein coding sequence of clone pw214\_15 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone pw214\_15 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID NO:44.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:43.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and
- (ab) the nucleotide sequence of the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 pw214\_15 deposited under accession number ATCC 98808;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:43 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43. Also preferably the



polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824, to a nucleotide  
5 sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:44;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
20 of SEQ ID NO:44, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID NO:44.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qb56\_19 deposited under accession  
30 number ATCC 98808;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qb56\_19 deposited under accession number ATCC 98808;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:46;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:45.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383; the nucleotide sequence of the full-length protein coding sequence of clone qb56\_19 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone qb56\_19 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:46, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:46.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:45.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and
- (ab) the nucleotide sequence of the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 qb56\_19 deposited under accession number ATCC 98808;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:45 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:46;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:46. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:46, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:46.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47;
  - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273;
  - (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273;
- 30 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qc646\_1 deposited under accession number ATCC 98808;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qc646\_1 deposited under accession number ATCC 98808;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:47.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273; the nucleotide sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273; the nucleotide sequence of the full-length protein coding sequence of clone qc646\_1 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone qc646\_1 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having

biological activity, the fragment comprising the amino acid sequence from amino acid 179 to amino acid 188 of SEQ ID NO:48.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:47.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

(ab) the nucleotide sequence of the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

(bb) the nucleotide sequence of the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

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ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:47 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:47. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;
- (b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
- (c) the amino acid sequence encoded by the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:48. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 179 to amino acid 188 of SEQ ID NO:48.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qf116\_2 deposited under accession number ATCC 98808;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qf116\_2 deposited under accession number ATCC 98808;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:50;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:49.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097; the nucleotide sequence of the full-length protein coding sequence of clone qf116\_2 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone qf116\_2 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein



comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 147 to amino acid 156 of SEQ ID NO:50.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:49.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

(ab) the nucleotide sequence of the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

(bb) the nucleotide sequence of the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:49 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:50;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:50. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 147 to amino acid 156 of SEQ ID NO:50.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qf662\_3 deposited under accession number ATCC 98808;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qf662\_3 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:52;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:51.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741; the nucleotide sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741; the nucleotide sequence of the full-length protein coding sequence of clone qf662\_3 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone qf662\_3 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808. In further preferred

embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a polynucleotide encoding  
5 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 92 to amino acid 101 of SEQ ID NO:52.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:51.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
15 consisting of:

(aa) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and

(ab) the nucleotide sequence of the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and

(bb) the nucleotide sequence of the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:51 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide  
10 741, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
15 NO:51 from nucleotide 595 to nucleotide 741, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741.

In other embodiments, the present invention provides a composition comprising  
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:52;
- (b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:52. In further preferred  
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 92 to amino acid 101 of SEQ ID NO:52.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone am748\_5 deposited under accession number ATCC 98817;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone am748\_5 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:54;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:53.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196; the nucleotide sequence of SEQ ID NO:53

from nucleotide 1002 to nucleotide 1196; the nucleotide sequence of the full-length protein coding sequence of clone am748\_5 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone am748\_5 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 40 to amino acid 49 of SEQ ID NO:54.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:53.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and
    - (ab) the nucleotide sequence of the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(bb) the nucleotide sequence of the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:53 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
15 corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196. Also preferably the polynucleotide isolated according to the above  
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:54;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and

(c) the amino acid sequence encoded by the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:54. In further preferred



embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 40 to amino acid 49 of SEQ ID NO:54.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide 1310;
- 15 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cj507\_1 deposited under accession number ATCC 98817;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cj507\_1 deposited under accession number ATCC 98817;
- 20 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:56;
- 25 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 30 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:55.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide 1310; the nucleotide sequence of the full-length protein coding sequence of clone cj507\_1 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cj507\_1 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 205 to amino acid 214 of SEQ ID NO:56.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:55.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

(ab) the nucleotide sequence of the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

(bb) the nucleotide sequence of the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55, and  
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide  
20 1310, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide 1310, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide 1310.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:56;

(b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:56. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 205 to amino acid 214 of SEQ ID NO:56.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide 1328;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cn922\_5 deposited under accession number ATCC 98817;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cn922\_5 deposited under accession number ATCC 98817;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:58;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:57.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide 1328; the nucleotide sequence of the full-length protein coding sequence of clone cn922\_5 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cn922\_5 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 184 to amino acid 193 of SEQ ID NO:58.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:57.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and
    - (ab) the nucleotide sequence of the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and

(bb) the nucleotide sequence of the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57, and  
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:57 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide  
20 1328, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide 1328, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide 1328.

In other embodiments, the present invention provides a composition comprising  
25 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:58;

(b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:58. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 184 to amino acid 193 of SEQ ID NO:58.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw691\_11 deposited under accession number ATCC 98817;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw691\_11 deposited under accession number ATCC 98817;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:60;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:59.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942; the nucleotide sequence of the full-length protein coding sequence of clone cw691\_11 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cw691\_11 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 139 to amino acid 148 of SEQ ID NO:60.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:59.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and
    - (ab) the nucleotide sequence of the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and



(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and

(bb) the nucleotide sequence of the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59, and  
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:59 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide  
20 942, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942.

In other embodiments, the present invention provides a composition comprising  
25 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:60;

(b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:60. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence  
5 from amino acid 139 to amino acid 148 of SEQ ID NO:60.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw1000\_2 deposited under accession  
15 number ATCC 98817;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817;
- (f) a polynucleotide comprising the nucleotide sequence of a mature  
20 protein coding sequence of clone cw1000\_2 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817;
- (h) a polynucleotide encoding a protein comprising the amino acid  
25 sequence of SEQ ID NO:62;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of  
30 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:61.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252; the nucleotide sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252; the nucleotide sequence of the full-length protein coding sequence of clone cw1000\_2 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cw1000\_2 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 202 to amino acid 211 of SEQ ID NO:62.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:61.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(ab) the nucleotide sequence of the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(bb) the nucleotide sequence of the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:61 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:62;

(b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and

(c) the amino acid sequence encoded by the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:62. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:62, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 202 to amino acid 211 of SEQ ID NO:62.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw1640\_1 deposited under accession number ATCC 98817;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw1640\_1 deposited under accession number ATCC 98817;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:64;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:63.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296; the nucleotide sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296; the nucleotide sequence of the full-length protein coding sequence of clone cw1640\_1 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cw1640\_1 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:64, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 203 to amino acid 212 of SEQ ID NO:64.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:63.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

(ab) the nucleotide sequence of the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

(bb) the nucleotide sequence of the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:63 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide

46 to nucleotide 1296. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:64;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:64. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:64, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 203 to amino acid 212 of SEQ ID NO:64.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 30 NO:65 from nucleotide 474 to nucleotide 827;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817;



(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:66;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:65.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827; the nucleotide sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827; the nucleotide sequence of the full-length protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the

fragment comprising the amino acid sequence from amino acid 122 to amino acid 131 of SEQ ID NO:66.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:65.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65; and

(ab) the nucleotide sequence of the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65; and

(bb) the nucleotide sequence of the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

5 ID NO:65 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:65 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:65. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:66;
- (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
- 20 (c) the amino acid sequence encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:66. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 122 to amino acid 131 of SEQ ID NO:66.

30 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529;

5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dd426\_1 deposited under accession number ATCC 98817;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817;

10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dd426\_1 deposited under accession number ATCC 98817;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817;

15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:68;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:68;

20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:67.

30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529; the nucleotide sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529; the nucleotide sequence of the full-length protein coding sequence of clone dd426\_1 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone dd426\_1 deposited under accession number ATCC 98817. In other preferred embodiments, the

polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:68.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:67.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and
    - (ab) the nucleotide sequence of the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and
    - (bb) the nucleotide sequence of the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:67 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67. Also preferably the  
10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide  
15 149 to nucleotide 529. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529, to a nucleotide sequence corresponding to the 3' end of  
20 said sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:68;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and
- (c) the amino acid sequence encoded by the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins. Preferably such  
30 protein comprises the amino acid sequence of SEQ ID NO:68. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:68 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:68.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
10 NO:69 from nucleotide 88 to nucleotide 543;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone di393\_2 deposited under accession number ATCC 98817;
- (e) a polynucleotide encoding the full-length protein encoded by the  
15 cDNA insert of clone di393\_2 deposited under accession number ATCC 98817;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone di393\_2 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA  
20 insert of clone di393\_2 deposited under accession number ATCC 98817;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:70;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment  
25 comprising eight contiguous amino acids of SEQ ID NO:70;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:69.

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Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543; the nucleotide sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543; the nucleotide sequence of the full-length protein coding sequence of clone di393\_2 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone di393\_2 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone di393\_2 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 80 to amino acid 89 of SEQ ID NO:70.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:69.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 25 (aa) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and
    - (ab) the nucleotide sequence of the cDNA insert of clone di393\_2 deposited under accession number ATCC 98817;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:



(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and
- (bb) the nucleotide sequence of the cDNA insert of clone di393\_2 deposited under accession number ATCC 98817;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 10 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:69 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543.

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In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

30

- (a) the amino acid sequence of SEQ ID NO:70;
- (b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and

(c) the amino acid sequence encoded by the cDNA insert of clone di393\_2 deposited under accession number ATCC 98817; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:70. In further preferred  
 5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising the amino acid sequence  
 10 from amino acid 80 to amino acid 89 of SEQ ID NO:70.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dj167\_2 deposited under accession number ATCC 98818;
- 20 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dj167\_2 deposited under accession number ATCC 98818;
- 25 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:72;
- (h) a polynucleotide encoding a protein comprising a fragment of the  
 30 amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:72;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:71.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356; the nucleotide sequence of the full-length  
10 protein coding sequence of clone dj167\_2 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone dj167\_2 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818. In further preferred  
15 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having  
20 biological activity, the fragment comprising the amino acid sequence from amino acid 195 to amino acid 204 of SEQ ID NO:72.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:71.

Further embodiments of the invention provide isolated polynucleotides produced  
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and  
(ab) the nucleotide sequence of the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

(bb) the nucleotide sequence of the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71, and  
20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:71 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71 from nucleotide  
25 1356, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356.

30 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:72;

(b) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and

(c) the amino acid sequence encoded by the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:72. In further preferred  
 5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence  
 10 from amino acid 195 to amino acid 204 of SEQ ID NO:72.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID  
 20 NO:73 from nucleotide 3645 to nucleotide 4343;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dj167\_19 deposited under accession number ATCC 207090;
- (f) a polynucleotide encoding the full-length protein encoded by the  
 25 cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dj167\_19 deposited under accession number ATCC 207090;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA  
 30 insert of clone dj167\_19 deposited under accession number ATCC 207090;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:74;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;

5 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

10 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:73.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490; the nucleotide sequence of SEQ ID NO:73  
15 from nucleotide 1485 to nucleotide 4490; the nucleotide sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343; the nucleotide sequence of the full-length protein coding sequence of clone dj167\_19 deposited under accession number ATCC 207090; or the nucleotide sequence of a mature protein coding sequence of clone dj167\_19 deposited under accession number ATCC 207090. In other preferred embodiments, the  
20 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:74 from amino acid 637 to amino acid 1036. In further preferred embodiments, the present invention provides a  
25 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid  
30 sequence from amino acid 513 to amino acid 522 of SEQ ID NO:74.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:73.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

(ab) the nucleotide sequence of the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090;

10 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

20 (bb) the nucleotide sequence of the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

25 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:73 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:73, but  
30 excluding the poly(A) tail at the 3' end of SEQ ID NO:73. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490, and extending contiguously from  
5 a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from  
10 nucleotide 3645 to nucleotide 4343, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343.

In other embodiments, the present invention provides a composition comprising  
15 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:74;
- (b) the amino acid sequence of SEQ ID NO:74 from amino acid 637 to amino acid 1036;
- 20 (c) a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74; and
- (d) the amino acid sequence encoded by the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090;

the protein being substantially free from other mammalian proteins. Preferably such  
25 protein comprises the amino acid sequence of SEQ ID NO:74 or the amino acid sequence of SEQ ID NO:74 from amino acid 637 to amino acid 1036. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
30 of SEQ ID NO:74, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence from amino acid 513 to amino acid 522 of SEQ ID NO:74.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:



- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dw665\_4 deposited under accession number ATCC 98818;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dw665\_4 deposited under accession number ATCC 98818;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:76;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:75.
- 30

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441; the nucleotide sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441; the nucleotide sequence of the full-length protein coding sequence of clone dw665\_4 deposited under accession number ATCC 98818; or the

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nucleotide sequence of a mature protein coding sequence of clone dw665\_4 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818. In further preferred  
5 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having  
10 biological activity, the fragment comprising the amino acid sequence from amino acid 223 to amino acid 232 of SEQ ID NO:76.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:75.

Further embodiments of the invention provide isolated polynucleotides produced  
15 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:  
20 (aa) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and  
(ab) the nucleotide sequence of the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;
  - (ii) hybridizing said probe(s) to human genomic DNA in  
25 conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:  
30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
  - (ba) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(bb) the nucleotide sequence of the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:75 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:76;

(b) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and

(c) the amino acid sequence encoded by the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:76. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 223 to amino acid 232 of SEQ ID NO:76.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
10 NO:77 from nucleotide 78 to nucleotide 1592;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dx146\_12 deposited under accession number ATCC 98818;
- (d) a polynucleotide encoding the full-length protein encoded by the  
15 cDNA insert of clone dx146\_12 deposited under accession number ATCC 98818;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dx146\_12 deposited under accession number ATCC 98818;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA  
20 insert of clone dx146\_12 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78;
- (h) a polynucleotide encoding a protein comprising a fragment of the  
25 amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein  
of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any  
30 one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:77.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592; the nucleotide sequence of the full-length protein coding sequence of clone dx146\_12 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone dx146\_12 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dx146\_12 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 247 to amino acid 256 of SEQ ID NO:78.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:77.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and
    - (ab) the nucleotide sequence of the cDNA insert of clone dx146\_12 deposited under accession number ATCC 98818;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

(bb) the nucleotide sequence of the cDNA insert of clone dx146\_12 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:77 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:78;

(b) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and

(c) the amino acid sequence encoded by the cDNA insert of clone dx146\_12 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:78. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 247 to amino acid 256 of SEQ ID NO:78.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79;

10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948;

15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dx219\_13 deposited under accession number ATCC 98818;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818;

20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dx219\_13 deposited under accession number ATCC 98818;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:80;

25 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

30 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:79.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948; the nucleotide sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948; the nucleotide sequence of the full-length protein coding sequence of clone dx219\_13 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone dx219\_13 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 150 to amino acid 159 of SEQ ID NO:80.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:79.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

(ab) the nucleotide sequence of the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);



and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

(bb) the nucleotide sequence of the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:80;

(b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and

(c) the amino acid sequence encoded by the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:80. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:80, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 150 to amino acid 159 of SEQ ID NO:80.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fm3\_1 deposited under accession number ATCC 98818;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fm3\_1 deposited under accession number ATCC 98818;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:82;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:82;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:81.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286; the nucleotide sequence of SEQ ID NO:81 from  
 15 nucleotide 62 to nucleotide 286; the nucleotide sequence of the full-length protein coding sequence of clone fm3\_1 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone fm3\_1 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fm3\_1  
 20 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:82, or a polynucleotide encoding a protein comprising a  
 25 fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:82.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:81.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(ab) the nucleotide sequence of the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(bb) the nucleotide sequence of the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:81 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide

5 to nucleotide 286. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:82;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:82. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:82, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:82.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 30 NO:83 from nucleotide 333 to nucleotide 572;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone h225\_1 deposited under accession number ATCC 98818;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone h225\_1 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:84;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:84;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:83.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572; the nucleotide sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572; the nucleotide sequence of the full-length protein coding sequence of clone h225\_1 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone h225\_1 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:84, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the

fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:84.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:83.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:83; and

(ab) the nucleotide sequence of the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:83; and

(bb) the nucleotide sequence of the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:83 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:83. Also preferably the polynucleotide isolated according to the above process comprises a

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nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:84;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:84. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 25 of SEQ ID NO:84, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:84.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210;



(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone kj320\_1 deposited under accession number ATCC 98818;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone kj320\_1 deposited under accession number ATCC 98818;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:86;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:86;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:85.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210; the nucleotide sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210; the nucleotide sequence of the full-length protein coding sequence of clone kj320\_1 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone kj320\_1 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818. In further preferred

embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:86, or a polynucleotide encoding  
5 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 465 to amino acid 474 of SEQ ID NO:86.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:85.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
15 consisting of:

(aa) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

(ab) the nucleotide sequence of the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

(bb) the nucleotide sequence of the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;

30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:85 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85 from nucleotide  
10 391 to nucleotide 3210, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
15 NO:85 from nucleotide 505 to nucleotide 3210, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210.

In other embodiments, the present invention provides a composition comprising  
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:86;
- (b) a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:86. In further preferred  
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:86, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 465 to amino acid 474 of SEQ ID NO:86.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ml236\_5 deposited under accession number ATCC 98818;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ml236\_5 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:88;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:87.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899; the nucleotide sequence of SEQ ID NO:87

from nucleotide 522 to nucleotide 899; the nucleotide sequence of the full-length protein coding sequence of clone ml236\_5 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone ml236\_5 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:88.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:87.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and

(ab) the nucleotide sequence of the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and

(bb) the nucleotide sequence of the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:87 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
15 corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899. Also preferably the polynucleotide isolated according to the above  
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:88;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and

(c) the amino acid sequence encoded by the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:88. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:88.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pu282\_10 deposited under accession number ATCC 98818;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pu282\_10 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:90;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:90;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:89.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452; the nucleotide sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452; the nucleotide sequence of the full-length protein coding sequence of clone pu282\_10 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone pu282\_10 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 69 to amino acid 78 of SEQ ID NO:90.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:89.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

(ab) the nucleotide sequence of the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and



(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

10 (bb) the nucleotide sequence of the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:89 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:89, but  
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:89. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452, to a nucleotide  
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from  
30 nucleotide 399 to nucleotide 452, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:90;
- (b) a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:90. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably  
 10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 69 to amino acid 78 of SEQ ID NO:90.

In one embodiment, the present invention provides a composition comprising an  
 15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179;
- 20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone at94\_2 deposited under accession number ATCC 98822;
- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone at94\_2 deposited under accession number ATCC 98822;
- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:92;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:92;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:91.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179; the nucleotide sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179; the nucleotide sequence of the full-length protein coding sequence of clone at94\_2 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone at94\_2 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 191 to amino acid 200 of SEQ ID NO:92.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:91.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and

(ab) the nucleotide sequence of the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and

(bb) the nucleotide sequence of the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:91 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide

4 to nucleotide 1179. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:92;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:92. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:92, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 191 to amino acid 200 of SEQ ID NO:92.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bf169\_13 deposited under accession number ATCC 98822;
- 30 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bf169\_13 deposited under accession number ATCC 98822;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:94;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:93.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077; the nucleotide sequence of the full-length protein coding sequence of clone bf169\_13 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone bf169\_13 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 332 to amino acid 341 of SEQ ID NO:94.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:93.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and
- (ab) the nucleotide sequence of the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 bf169\_13 deposited under accession number ATCC 98822;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:93 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:94;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:94. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:94, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 332 to amino acid 341 of SEQ ID NO:94.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bl152\_12 deposited under accession number ATCC 98822;
- 30 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bl152\_12 deposited under accession number ATCC 98822;



(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bl152\_12 deposited under accession number ATCC 98822;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bl152\_12 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:96;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:96;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:95.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735; the nucleotide sequence of the full-length protein coding sequence of clone bl152\_12 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone bl152\_12 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bl152\_12 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 97 to amino acid 106 of SEQ ID NO:96.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:95.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:95, but excluding the poly(A) tail at the
- 10 3' end of SEQ ID NO:95; and
- (ab) the nucleotide sequence of the cDNA insert of clone bl152\_12 deposited under accession number ATCC 98822;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 bl152\_12 deposited under accession number ATCC 98822;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:95 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:96;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone bl152\_12 deposited under accession number ATCC 98822;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:96. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:96, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 97 to amino acid 106 of SEQ ID NO:96.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bz578\_1 deposited under accession
- 30 number ATCC 98822;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822;

- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bz578\_1 deposited under accession number ATCC 98822;
  - (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822;
  - (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:98;
  - (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:98;
  - (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
  - (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
  - (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
  - (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:97.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816; the nucleotide sequence of the full-length protein coding sequence of clone bz578\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone bz578\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:98.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:97.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and
- (ab) the nucleotide sequence of the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 bz578\_1 deposited under accession number ATCC 98822;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:97 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:98;
- (b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and
- (c) the amino acid sequence encoded by the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:98. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:98, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:98.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 30 NO:99 from nucleotide 765 to nucleotide 992;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cb123\_1 deposited under accession number ATCC 98822;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cb123\_1 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:100;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:100;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:99.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992; the nucleotide sequence of SEQ ID NO:99 from nucleotide 765 to nucleotide 992; the nucleotide sequence of the full-length protein coding sequence of clone cb123\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone cb123\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:100, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100

having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:100.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:99.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

(ab) the nucleotide sequence of the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

(bb) the nucleotide sequence of the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ



5 ID NO:99 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:99 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:99. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99 from nucleotide 765 to nucleotide 992, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:99 from nucleotide 765 to nucleotide 992, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:99 from nucleotide 765 to nucleotide 992.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:100;
- (b) a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100; and
- 20 (c) the amino acid sequence encoded by the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:100. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:100, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:100.

30 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ch245\_1 deposited under accession number ATCC 98822;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ch245\_1 deposited under accession number ATCC 98822;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:102;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:101.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480; the nucleotide sequence of the full-length protein coding sequence of clone ch245\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone ch245\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102  
5 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:102.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:101.

Further embodiments of the invention provide isolated polynucleotides produced  
10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and

(ab) the nucleotide sequence of the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and

30 (bb) the nucleotide sequence of the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:101 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:102;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:102. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:102.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cj378\_3 deposited under accession number ATCC 98822;

5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cj378\_3 deposited under accession number ATCC 98822;

10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:104;

15 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

20 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:103.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541; the nucleotide sequence of the full-length protein coding sequence of clone cj378\_3 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone cj378\_3 deposited under accession number ATCC 98822. In other preferred embodiments, the  
30 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:104, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:104.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:103.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and
    - 15 (ab) the nucleotide sequence of the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 20 and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
  - 25 the group consisting of:
    - (ba) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and
    - (bb) the nucleotide sequence of the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822;
  - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:103 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:104;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:104. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:104, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:104.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw1481\_1 deposited under accession number ATCC 98822;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw1481\_1 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:106;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:105.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202; the nucleotide sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349; the nucleotide sequence of the full-length protein coding sequence of clone cw1481\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone cw1481\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822. In further preferred



embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a polynucleotide  
5 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 264 to amino acid 273 of SEQ ID NO:106.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:105.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
15 consisting of:

(aa) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

(ab) the nucleotide sequence of the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

(bb) the nucleotide sequence of the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822;

30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:105 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide  
10 2202, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
15 NO:105 from nucleotide 401 to nucleotide 2349, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349.

In other embodiments, the present invention provides a composition comprising  
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:106;
- (b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:106. In further preferred embodiments, the present invention provides a protein comprising a fragment of the  
30 amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 264 to amino acid 273 of SEQ ID NO:106.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dd119\_4 deposited under accession number ATCC 98822;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dd119\_4 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:108;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:108;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:107.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905; the nucleotide sequence of SEQ ID NO:107

from nucleotide 146 to nucleotide 2905; the nucleotide sequence of the full-length protein coding sequence of clone dd119\_4 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone dd119\_4 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:108, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 474 to amino acid 483 of SEQ ID NO:108.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:107.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and

(ab) the nucleotide sequence of the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and

(bb) the nucleotide sequence of the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:107 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

15 corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905. Also preferably the polynucleotide isolated according to the above

20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:108;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108; and

(c) the amino acid sequence encoded by the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:108. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:108, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 474 to amino acid 483 of SEQ ID NO:108.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone df202\_3 deposited under accession number ATCC 98822;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone df202\_3 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:110;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:110;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:109.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369; the nucleotide sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369; the nucleotide sequence of the full-length protein coding sequence of clone df202\_3 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone df202\_3 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:110, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:110.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:109.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

(ab) the nucleotide sequence of the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

10 (bb) the nucleotide sequence of the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:109 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:109, but  
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:109. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369, to a nucleotide  
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from  
30 nucleotide 103 to nucleotide 369, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:



- (a) the amino acid sequence of SEQ ID NO:110;
- (b) a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110; and
- (c) the amino acid sequence encoded by the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:110. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably  
10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:110, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:110.

In one embodiment, the present invention provides a composition comprising an  
15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539;
- 20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone km225\_1 deposited under accession number ATCC 98822;
- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone km225\_1 deposited under accession number ATCC 98822;
- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:112;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:111.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539; the nucleotide sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539; the nucleotide sequence of the full-length protein coding sequence of clone km225\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone km225\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:112.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:111.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

(ab) the nucleotide sequence of the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

(bb) the nucleotide sequence of the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:111 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111

from nucleotide 2192 to nucleotide 2539. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said  
5 sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
10 consisting of:

- (a) the amino acid sequence of SEQ ID NO:112;
- (b) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and
- (c) the amino acid sequence encoded by the cDNA insert of clone  
15 km225\_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:112. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably  
20 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:112.

In one embodiment, the present invention provides a composition comprising an  
25 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 1734 to nucleotide 2030;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
30 NO:113 from nucleotide 1965 to nucleotide 2030;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone mj301\_1 deposited under accession number ATCC 98822;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone mj301\_1 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:114;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:114;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:113.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:113 from nucleotide 1734 to nucleotide 2030; the nucleotide sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030; the nucleotide sequence of the full-length protein coding sequence of clone mj301\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone mj301\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114

having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:114.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:113.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and

(ab) the nucleotide sequence of the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and

25 (bb) the nucleotide sequence of the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

15            In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:114;  
(b) a fragment of the amino acid sequence of SEQ ID NO:114, the  
fragment comprising eight contiguous amino acids of SEQ ID NO:114; and  
(c) the amino acid sequence encoded by the cDNA insert of clone  
mj301\_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:114. In further preferred  
25 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a protein comprising a fragment of the amino acid sequence of SEQ  
ID NO:114 having biological activity, the fragment comprising the amino acid sequence  
30 from amino acid 44 to amino acid 53 of SEQ ID NO:114.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350;

5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ml10\_7 deposited under accession number ATCC 98822;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;

10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ml10\_7 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;

15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:116;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:116;

20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:115.

30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350; the nucleotide sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350; the nucleotide sequence of the full-length protein coding sequence of clone ml10\_7 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone ml10\_7 deposited under accession number ATCC 98822. In other preferred embodiments, the



polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:116, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 87 to amino acid 96 of SEQ ID NO:116.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:115.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and
- 20 (ab) the nucleotide sequence of the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- 25

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 30 (ba) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and
- (bb) the nucleotide sequence of the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:115 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115. Also preferably the

10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:115 from nucleotide

15 799 to nucleotide 1350. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350, to a nucleotide sequence corresponding to the 3' end

20 of said sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:116;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such

30 protein comprises the amino acid sequence of SEQ ID NO:116. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:116, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 87 to amino acid 96 of SEQ ID NO:116.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone my340\_1 deposited under accession  
10 number ATCC 98822;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone my340\_1 deposited under accession number ATCC 98822;
- (e) a polynucleotide comprising the nucleotide sequence of a mature  
15 protein coding sequence of clone my340\_1 deposited under accession number ATCC 98822;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone my340\_1 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a protein comprising the amino acid  
20 sequence of SEQ ID NO:118;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:118;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of  
25 (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:117.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094; the nucleotide sequence of the full-length

protein coding sequence of clone my340\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone my340\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone my340\_1 deposited under accession number ATCC 98822. In further preferred  
5       embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:118, or a polynucleotide  
10       encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:118.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:117.

15       Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a)     a process comprising the steps of:

(i)     preparing one or more polynucleotide probes that hybridize  
20       in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa)    SEQ ID NO:117, but excluding the poly(A) tail at the  
3' end of SEQ ID NO:117; and

(ab)    the nucleotide sequence of the cDNA insert of clone  
my340\_1 deposited under accession number ATCC 98822;

25       (ii)    hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii)   isolating the DNA polynucleotides detected with the  
probe(s);

and

30       (b)     a process comprising the steps of:

(i)     preparing one or more polynucleotide primers that  
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from  
the group consisting of:

(ba) SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117; and

(bb) the nucleotide sequence of the cDNA insert of clone my340\_1 deposited under accession number ATCC 98822;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:117 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
15 corresponding to the cDNA sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:118;

(b) a fragment of the amino acid sequence of SEQ ID NO:118, the  
25 fragment comprising eight contiguous amino acids of SEQ ID NO:118; and

(c) the amino acid sequence encoded by the cDNA insert of clone my340\_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:118. In further preferred  
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:118, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:118.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial, yeast, insect and mammalian cells, transformed with such polynucleotide compositions. Also provided by the present invention are organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise:

- (a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and
- (b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present invention.

Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

#### BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

#### DETAILED DESCRIPTION

##### ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone in accordance with known methods. The predicted amino acid sequence (both full-length and mature forms) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by

expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing.

5 As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins  
10 which are transported across the membrane of the endoplasmic reticulum.

#### Clone "bn365\_53"

A polynucleotide of the present invention has been identified as clone "bn365\_53". bn365\_53 was isolated from a human adult placenta cDNA library using methods which  
15 are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bn365\_53 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bn365\_53 protein").

20 The nucleotide sequence of bn365\_53 as presently determined is reported in SEQ ID NO:1, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bn365\_53 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
25 bn365\_53 should be approximately 650 bp.

The nucleotide sequence disclosed herein for bn365\_53 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bn365\_53 demonstrated at least some similarity with sequences identified as AA242967 (zr65g11.r1 Soares NhHMPu S1 Homo sapiens cDNA clone  
30 668324 5') and N40141 (yw73c12.r1 Homo sapiens cDNA clone 257878 5'). The predicted amino acid sequence disclosed herein for bn365\_53 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bn365\_53 protein demonstrated at least some similarity to sequences identified as D63484 (KIAA0150 protein [Homo sapiens]) and to the GAGE-1 to GAGE-6 family of

human proteins expressed in tumors (GenBank Accession Numbers U19142-U19147). The amino acid sequence of SEQ ID NO:2 contains two RGD (Arg-Gly-Asp) motifs (around residues 12 and 75): the sequence Arg-Gly-Asp, found in fibronectin, is crucial for its interaction with its cell surface receptor, an integrin. What has been called the 'RGD' tripeptide is also found in the sequences of a number of other proteins, where it has been shown to play a role in cell adhesion. These proteins are: some forms of collagens, fibrinogen, vitronectin, von Willebrand factor (VWF), snake disintegrins, and slime mold discoidins. Based upon sequence similarity, bn365\_53 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of bn365\_53 indicates that it may contain one or more repetitive elements.

#### Clone "bo342\_2"

A polynucleotide of the present invention has been identified as clone "bo342\_2". bo342\_2 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bo342\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bo342\_2 protein").

The nucleotide sequence of bo342\_2 as presently determined is reported in SEQ ID NO:3, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bo342\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:4. Amino acids 372 to 384 of SEQ ID NO:4 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 385. Amino acids 1 to 13 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning in that case at amino acid 14. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the bo342\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bo342\_2 should be approximately 2600 bp.

The nucleotide sequence disclosed herein for bo342\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bo342\_2 demonstrated at least some similarity with sequences



identified as AA306000 (EST177027 Jurkat T-cells VI Homo sapiens cDNA 5' end) and W94256 (ze12b02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358731 3' similar to contains Alu repetitive element). Based upon sequence similarity, bo342\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts six potential transmembrane domains within the bo342\_2 protein sequence, centered around amino acids 300, 320, 380, 410, 430, and 490 of SEQ ID NO:4, respectively. The nucleotide sequence of bo342\_2 indicates that it may contain Alu or other repetitive elements.

10        Clone "dn721\_8"

A polynucleotide of the present invention has been identified as clone "dn721\_8". dn721\_8 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dn721\_8 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dn721\_8 protein").

The nucleotide sequence of dn721\_8 as presently determined is reported in SEQ ID NO:5, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dn721\_8 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:6.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dn721\_8 should be approximately 2900 bp.

The nucleotide sequence disclosed herein for dn721\_8 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dn721\_8 demonstrated at least some similarity with sequences identified as H63637 (yr34b12.r1 Homo sapiens cDNA clone 207167 5'), N31598 (yy20b12.s1 Homo sapiens cDNA clone 271775 3'), and R61419 (yh15e05.r1 Homo sapiens cDNA clone 37671 5'). Based upon sequence similarity, dn721\_8 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two possible transmembrane domains within the dn721\_8 protein sequence, one centered around amino acid 269 and another around amino acid 457 of SEQ ID NO:6.

Clone "dn834\_1"

A polynucleotide of the present invention has been identified as clone "dn834\_1". dn834\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dn834\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dn834\_1 protein").

The nucleotide sequence of dn834\_1 as presently determined is reported in SEQ  
10 ID NO:7, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dn834\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:8.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dn834\_1 should be approximately 900 bp.

15 The nucleotide sequence disclosed herein for dn834\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dn834\_1 demonstrated at least some similarity with sequences identified as AA544005 (vj83h07.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone 935677 5'), AL022163 (Human DNA sequence \*\*\* SEQUENCING  
20 IN PROGRESS \*\*\* from clone 551E13; HTGS phase 1), L44560 (Homo sapiens thymus mRNA (randomly primed, normalized), single-pass sequence), and T72271 (Human B cell surface antigen cDNA). The predicted amino acid sequence disclosed herein for dn834\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dn834\_1 protein demonstrated at least some  
25 similarity to sequences identified as R47496 (Translated sequence of domains I and II of celD cDNA in clone pCNP4). Based upon sequence similarity, dn834\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the dn834\_1 protein sequence, centered around amino acids 59, 84, and 145 of SEQ ID NO:8, respectively.

30 dn834\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 18 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "pd278\_5"

A polynucleotide of the present invention has been identified as clone "pd278\_5". A cDNA clone was first isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or  
5 was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate pd278\_5 from a human adult kidney cDNA library. pd278\_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pd278\_5 protein").

10 The nucleotide sequence of pd278\_5 as presently determined is reported in SEQ ID NO:9, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pd278\_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:10. Amino acids 61 to 73 of SEQ ID NO:10 are a predicted leader/signal sequence, with the predicted  
15 mature amino acid sequence beginning at amino acid 74. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pd278\_5 protein.

There are two additional and mutually overlapping possible open reading frames  
20 close to the 5' end of SEQ ID NO:9 (bases 82 - 420 and bases 119 - 414). The translated open reading frame of bases 119 - 414 has a predicted leader/signal sequence from amino acid 49 to amino acid 61, with the predicted mature amino acid sequence beginning at amino acid 62. Each of the additional possible open reading frames has a predicted transmembrane domain.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pd278\_5 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for pd278\_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pd278\_5 demonstrated at least some similarity with sequences  
30 identified as AA292241 (zt50d11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 725781 5'), AA428245 zw51d10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773587 3'), AA599487 (ag23f05.s1 Jia bone marrow stroma Homo sapiens cDNA clone 1071201 3'), AA827135 (ob53b03.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE 1335053 3'), H54322 (yq90d03.s1 Homo sapiens cDNA clone 203045 3'), and

669050" 1190E50  
T22170 (Human gene signature HUMGS03741). The predicted amino acid sequence disclosed herein for pd278\_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pd278\_5 protein demonstrated at least some similarity to sequences identified as R13144 (Deleted in  
5 Colorectal Carcinomas) and X13885 (extensin (AA 1-620) [Nicotiana tabacum]). Based upon sequence similarity, pd278\_5 proteins and each similar protein or peptide may share at least some activity.

Clone "pe80\_1"

10 A polynucleotide of the present invention has been identified as clone "pe80\_1". pe80\_1 was isolated from a human adult blood (chronic myelogenous leukemia K562) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded  
15 protein. pe80\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pe80\_1 protein").

The nucleotide sequence of pe80\_1 as presently determined is reported in SEQ ID NO:11, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pe80\_1 protein corresponding  
20 to the foregoing nucleotide sequence is reported in SEQ ID NO:12.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pe80\_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for pe80\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
25 FASTA search protocols. pe80\_1 demonstrated at least some similarity with sequences identified as AA291078 (zs47b04.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:700591 5'), AA429912 (zw66e06.s1 Soares testis NHT Homo sapiens cDNA clone 781186 3'), H82367 (yv79d06.r1 Homo sapiens cDNA clone 248939 5' similar to contains Alu repetitive element; contains OFR repetitive element), Q60627 (Human brain Expressed  
30 Sequence Tag EST02640), and R20261 (yg20a02.r1 Homo sapiens cDNA clone 32587 5'). Based upon sequence similarity, pe80\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two possible transmembrane domains within the pe80\_1 protein sequence, one centered around amino

acid 58 and another around amino acid 109 of SEQ ID NO:12. The nucleotide sequence of pe80\_1 indicates that it may contain an Alu repetitive element.

Clone "pm113\_1"

5 A polynucleotide of the present invention has been identified as clone "pm113\_1". pm113\_1 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pm113\_1 is a  
10 full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm113\_1 protein").

The nucleotide sequence of pm113\_1 as presently determined is reported in SEQ ID NO:13, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pm113\_1 protein  
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:14. Amino acids 41 to 53 of SEQ ID NO:14 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 54. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the  
20 pm113\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm113\_1 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for pm113\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
25 FASTA search protocols. pm113\_1 demonstrated at least some similarity with sequences identified as AA009482 (zi04c03.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429796 5'), AA350890 (EST58401 Infant brain Homo sapiens cDNA 3' end), AC003030 (Human DNA from chromosome 19-specific cosmid R29828, genomic sequence, complete sequence), H98961 (yx11b02.s1 Homo sapiens cDNA clone 261387 3'), R07796  
30 (yf15e05.r1 Homo sapiens cDNA clone), T22151 (Human gene signature HUMGS03721), and W68491 (zd34h02.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 342579 5'). Based upon sequence similarity, pm113\_1 proteins and each similar protein or peptide may share at least some activity.

Clone "pm749\_8"

A polynucleotide of the present invention has been identified as clone "pm749\_8". pm749\_8 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pm749\_8 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm749\_8 protein").

The nucleotide sequence of pm749\_8 as presently determined is reported in SEQ ID NO:15, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pm749\_8 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm749\_8 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for pm749\_8 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pm749\_8 demonstrated at least some similarity with sequences identified as AA314025 (EST185879 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end) and AA374458 (EST86612 HSC172 cells I Homo sapiens cDNA 5' end). The predicted amino acid sequence disclosed herein for pm749\_8 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pm749\_8 protein demonstrated at least some similarity to sequences identified as D89169 (similar to Saccharomyces cerevisiae SCD6 protein, SWISS-PROT Accession Number P45978 [Schizosaccharomyces pombe]) and U30384 (Scd6p [Saccharomyces cerevisiae]). Based upon sequence similarity, pm749\_8 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pm749\_8 protein sequence centered around amino acid 138 of SEQ ID NO:16.

Clone "pt31\_4"

A polynucleotide of the present invention has been identified as clone "pt31\_4". pt31\_4 was isolated from a human adult blood (lymphoblastic leukemia MOLT-4) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on

the basis of computer analysis of the amino acid sequence of the encoded protein. pt31\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pt31\_4 protein").

5 The nucleotide sequence of pt31\_4 as presently determined is reported in SEQ ID NO:17, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pt31\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:18. Amino acids 19 to 31 of SEQ ID NO:18 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 32. Due to the hydrophobic nature of the  
10 predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pt31\_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pt31\_4 should be approximately 3200 bp.

15 The nucleotide sequence disclosed herein for pt31\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pt31\_4 demonstrated at least some similarity with sequences identified as AA348130 (EST54532 Fetal heart II Homo sapiens cDNA 5' end), AA350691 (EST58082 Infant brain Homo sapiens cDNA 5' end), AC001226 (Genomic sequence from  
20 Human 13, complete sequence), H22773 (ym54c06.r1 Homo sapiens cDNA clone 52351 5'), and R21869 (yh22b10.s1 Homo sapiens cDNA clone 130459 3'). The predicted amino acid sequence disclosed herein for pt31\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pt31\_4 protein demonstrated at least some similarity to sequences identified as U53147 (C01B7.6  
25 [Caenorhabditis elegans]). Based upon sequence similarity, pt31\_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five potential transmembrane domains within the pt31\_4 protein sequence, centered around amino acids 90, 110, 210, 410, and 590 of SEQ ID NO:18, respectively.

30

#### Clone "pv296\_5"

A polynucleotide of the present invention has been identified as clone "pv296\_5". pv296\_5 was isolated from a human adult brain (cerebellum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or

was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pv296\_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pv296\_5 protein").

5       The nucleotide sequence of pv296\_5 as presently determined is reported in SEQ ID NO:19, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pv296\_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:20.

10       The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pv296\_5 should be approximately 1800 bp.

15       The nucleotide sequence disclosed herein for pv296\_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pv296\_5 demonstrated at least some similarity with sequences identified as AA022471 (ze70c01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 364320 3'), AA335246 (EST39647 Epididymus Homo sapiens cDNA 5' end), and AA481308 (zv06a05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 752816 5'). Based upon sequence similarity, pv296\_5 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pv296\_5 protein sequence centered around amino acid  
20   32 of SEQ ID NO:20.

#### Clone "er311\_20"

25       A polynucleotide of the present invention has been identified as clone "er311\_20". er311\_20 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. er311\_20 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "er311\_20 protein").

30       The nucleotide sequence of er311\_20 as presently determined is reported in SEQ ID NO:21, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the er311\_20 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:22. Amino acids 654 to 666 of SEQ ID NO:22 are a possible leader/signal sequence, with the



predicted mature amino acid sequence beginning at amino acid 667. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the er311\_20 protein.

5           The EcoRI/NotI restriction fragment obtainable from the deposit containing clone er311\_20 should be approximately 2800 bp.

          The nucleotide sequence disclosed herein for er311\_20 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. er311\_20 demonstrated at least some similarity with sequences  
10 identified as AF035526 (Mus musculus kanadaplin mRNA, complete cds), R18277 (yg01c06.r1 Homo sapiens cDNA clone 31018 5' similar to SP:ZK632.2 CE00419 COILED COIL PROTEIN), R47371 (Hf060-r Homo sapiens cDNA clone f060-r), and Z40133 (H. sapiens partial cDNA sequence; clone c-1sh08). The predicted amino acid sequence disclosed herein for er311\_20 was searched against the GenPept and GeneSeq  
15 amino acid sequence databases using the BLASTX search protocol. The predicted er311\_20 protein demonstrated at least some similarity to sequences identified as AF035526 (kanadaplin [Mus musculus]) and Z22181 (ZK632.2 [Caenorhabditis elegans]). The mouse kanadaplin protein and the predicted er311\_20 protein both contain polyglutamic acid stretches within their C-terminal portions. Based upon sequence similarity,  
20 er311\_20 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the er311\_20 protein sequence, one centered around amino acid 667 and another at the extreme C-terminus of SEQ ID NO:22.

          er311\_20 protein was expressed in a COS cell expression system, and an expressed  
25 protein band of approximately 91 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "fh149\_12"

          A polynucleotide of the present invention has been identified as clone "fh149\_12".  
30 fh149\_12 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fh149\_12 is a full-length

clone, including the entire coding sequence of a secreted protein (also referred to herein as "fh149\_12 protein").

The nucleotide sequence of fh149\_12 as presently determined is reported in SEQ ID NO:23, and includes a poly(A) tail. What applicants presently believe to be the proper  
5 reading frame and the predicted amino acid sequence of the fh149\_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:24. Amino acids 133 to 145 of SEQ ID NO:24 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 146. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a  
10 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the fh149\_12 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fh149\_12 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for fh149\_12 was searched against the  
15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fh149\_12 demonstrated at least some similarity with sequences identified as AA653557 (ag67b07.s1 Gessler Wilms tumor Homo sapiens cDNA clone 1127989 3'), AA191185 (zq45b09.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 632633 5'), H20588 (yn63d06.r1 Homo sapiens cDNA clone 173099 5'),  
20 R16294 (yf93b09.r1 Homo sapiens cDNA clone 30087 5'), T08702 (Rat OCT-1 gene), T25120 (Human gene signature HUMGS07278), U38652 (Mus musculus transmembrane transporter (Lx1) mRNA, complete cds), U77086 (Human organic cation transporter 1 (hOCT1) mRNA, complete cds), and Z66539 (H.sapiens creatine transporter gene). The predicted amino acid sequence disclosed herein for fh149\_12 was searched against the  
25 GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted fh149\_12 protein demonstrated at least some similarity to sequences identified as D17546 (Collagen [Mus musculus]), R77676 (Rat OCT-1 protein), and U77086 (organic cation transporter 1 [Homo sapiens]). The fh149\_12 protein also shows some homology to organic cation transporters from rat (GenBank L27651) and pig  
30 (GenBank Y09400) cells. Based upon sequence similarity, fh149\_12 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts eleven potential transmembrane domains within the fh149\_12 protein

sequence, centered around amino acids 40, 112, 139, 162, 200, 229, 349, 376, 405, 436, and 467 of SEQ ID NO:24, respectively.

Clone "pc201\_6"

5 A polynucleotide of the present invention has been identified as clone "pc201\_6". pc201\_6 was isolated from a human adult retina (retinoblastoma WERI-Rb1) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pc201\_6  
10 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pc201\_6 protein").

The nucleotide sequence of pc201\_6 as presently determined is reported in SEQ ID NO:25, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pc201\_6 protein  
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:26. Amino acids 20 to 32 of SEQ ID NO:26 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 33. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the  
20 pc201\_6 protein.

A partial cDNA clone related to pc201\_6, pc201\_SP, was also isolated from a human adult retina (retinoblastoma WERI-Rb1) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer  
25 analysis of the amino acid sequence of the encoded protein. The pc201\_SP clone appears to encode a splice variant of the pc201\_6 protein. The amino acid sequence of the predicted pc201\_SP splice variant protein comprises the amino acid sequence reported in SEQ ID NO:177.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
30 pc201\_6 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for pc201\_6 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pc201\_6 demonstrated at least some similarity with sequences identified as AA256414 (zr80d11.r1 Soares NhHMPu S1 Homo sapiens cDNA clone

682005 5' similar to WP EEED8.9 CE01893), AA342139 (EST47690 Fetal spleen Homo sapiens cDNA 3' end), AC004085 (Homo sapiens; HTGS phase 1, 72 unordered pieces), AF035950 (Homo sapiens putative DDB p127-associated protein mRNA, partial cds), and H10436 (ym08d09.s1 Homo sapiens cDNA clone 47394 3'). The predicted amino acid  
5 sequence disclosed herein for pc201\_6 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pc201\_6 protein demonstrated at least some similarity to sequences identified as AF035950 (putative DDB p127-associated protein [Homo sapiens]) and U23484 (EEED8.5 [Caenorhabditis elegans]). Based upon sequence similarity, pc201\_6 proteins and each  
10 similar protein or peptide may share at least some activity.

#### Clone "pl87\_1"

A polynucleotide of the present invention has been identified as clone "pl87\_1". pl87\_1 was isolated from a human fetal kidney (293 cell line) cDNA library using methods  
15 which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pl87\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pl87\_1 protein").

20 The nucleotide sequence of pl87\_1 as presently determined is reported in SEQ ID NO:27, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pl87\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
25 pl87\_1 should be approximately 700 bp.

The nucleotide sequence disclosed herein for pl87\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pl87\_1 demonstrated at least some similarity with sequences identified as AA371861 (EST83927 Parathyroid gland tumor I Homo sapiens cDNA 5' end)  
30 and AA861863 (ak39e11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1408364 3'). Based upon sequence similarity, pl87\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential

transmembrane domains within the pl87\_1 protein sequence centered around amino acid 50 of SEQ ID NO:28.

pl87\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 22 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "pm514\_4"

A polynucleotide of the present invention has been identified as clone "pm514\_4". pm514\_4 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pm514\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm514\_4 protein").

The nucleotide sequence of pm514\_4 as presently determined is reported in SEQ ID NO:29, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pm514\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:30.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm514\_4 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for pm514\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pm514\_4 demonstrated at least some similarity with sequences identified as AA393855 (zv64g11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 758468 5' similar to WP ZK1248.14 CE02898), AA427943 (zw53d10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773779 3'), AA434561 (zw53d10.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773779 5'), W49736 (zc41a03.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324844 5'), and U95822 (Human putative transmembrane GTPase mRNA, partial cds). The predicted amino acid sequence disclosed herein for pm514\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pm514\_4 protein demonstrated at least some similarity to sequences identified as U95822 (putative transmembrane GTPase [Homo sapiens]). Based upon sequence

similarity, pm514\_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pm514\_4 protein sequence, centered around amino acid 600 of SEQ ID NO:30.

5           Clone "co155\_12"

A polynucleotide of the present invention has been identified as clone "co155\_12". co155\_12 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer  
10 analysis of the amino acid sequence of the encoded protein. co155\_12 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "co155\_12 protein").

The nucleotide sequence of co155\_12 as presently determined is reported in SEQ ID NO:31, and includes a poly(A) tail. What applicants presently believe to be the proper  
15 reading frame and the predicted amino acid sequence of the co155\_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:32. Amino acids 21 to 33 of SEQ ID NO:32 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 34. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain  
20 should the predicted leader/signal sequence not be separated from the remainder of the co155\_12 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone co155\_12 should be approximately 2700 bp.

The nucleotide sequence disclosed herein for co155\_12 was searched against the  
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. co155\_12 demonstrated at least some similarity with sequences identified as AA578373 (nl23d11.s1 NCI\_CGAP\_HSC1 Homo sapiens cDNA clone IMAGE:1041525, mRNA sequence), N43800 (yy42h09.r1 Homo sapiens cDNA clone 273953 5'), and W40418 (zc82c10.r1 Pancreatic Islet Homo sapiens cDNA clone 328818  
30 5', mRNA sequence). The predicted amino acid sequence disclosed herein for co155\_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted co155\_12 protein demonstrated at least some similarity to the sequences identified as L12721 (transmembrane domain encoded by

1099-1167) and AF004849 (human serine/threonin protein kinase). Based upon sequence similarity, co155\_12 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional potential trans-membrane domains within the co155\_12 protein sequence, centered around amino acids  
5 90, 180, 470, 580, and 610 of SEQ ID NO:32, respectively.

#### Clone "fn189\_13"

A polynucleotide of the present invention has been identified as clone "fn189\_13". fn189\_13 was isolated from a human fetal brain cDNA library using methods which are  
10 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fn189\_13 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "fn189\_13 protein").

15 The nucleotide sequence of fn189\_13 as presently determined is reported in SEQ ID NO:33, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the fn189\_13 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:34. Amino acids 9 to 21 of SEQ ID NO:34 are a predicted leader/signal sequence, with the predicted  
20 mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the fn189\_13 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
25 fn189\_13 should be approximately 3800 bp.

The nucleotide sequence disclosed herein for fn189\_13 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fn189\_13 demonstrated at least some similarity with sequences identified as AA144270 (mr14d12.r1 Soares mouse 3NbMS Mus musculus cDNA clone  
30 597431 5') and N27605 (yx44e10.r1 Homo sapiens cDNA clone 264618 5'). The predicted amino acid sequence disclosed herein for fn189\_13 was searched against the GenPept, GeneSeq, and SWISS\_PROT amino acid sequence databases using the BLASTX search protocol. The predicted fn189\_13 protein demonstrated at least some similarity to

sequences identified as P32857 (PROTEIN PTM1 PRECURSOR [Saccharomyces cerevisiae]) and U64598 (weakly similar to S. cerevisiae PTM1 precursor (SP:P32857) [Caenorhabditis elegans]). Based upon sequence similarity, fn189\_13 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional potential transmembrane domains within the fn189\_13 protein sequence, centered around amino acids 225, 260, 340, 360, and 420 of SEQ ID NO:34, respectively.

#### Clone "lv2\_47"

A polynucleotide of the present invention has been identified as clone "lv2\_47". lv2\_47 was isolated from a human adult thyroid cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. lv2\_47 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "lv2\_47 protein").

The nucleotide sequence of lv2\_47 as presently determined is reported in SEQ ID NO:35, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the lv2\_47 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:36. The TopPredII computer program predicts a potential transmembrane domain within the lv2\_47 protein sequence of SEQ ID NO:36, centered around amino acid 60.

Another potential lv2\_47 reading frame and predicted amino acid sequence is encoded by basepairs 365 to 880 of SEQ ID NO:35 and is reported in SEQ ID NO:178. Amino acids 49 to 61 of SEQ ID NO:178 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 62. Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO:178. The TopPredII computer program predicts two additional potential transmembrane domains within the SEQ ID NO:178 amino acid sequence.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone lv2\_47 should be approximately 1950 bp.

The nucleotide sequence disclosed herein for lv2\_47 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and



FASTA search protocols. lv2\_47 demonstrated at least some similarity with sequences identified as AA007293 (zh97f07.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429253 5'), AA447347 (zw93g06.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784570 5' similar to WP:F43E2.7 CE07243), AA522451 (ng30h09.s1  
5 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:936353), AA526614 (ni52g12.s1 NCI\_CGAP\_Ov2 Homo sapiens cDNA clone 980518), F18178 (H.sapiens EST sequence (002-T4-28) from skeletal muscle, mRNA sequence), H46569 (yo20f10.s1 Homo sapiens cDNA clone 178507 3'), and T22574 (Human gene signature HUMGS04190). Based upon sequence similarity, lv2\_47 proteins and each similar protein or peptide may share  
10 at least some activity.

#### Clone "ml243\_1"

A polynucleotide of the present invention has been identified as clone "ml243\_1". ml243\_1 was isolated from a human adult brain (caudate nucleus) cDNA library using  
15 methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ml243\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ml243\_1 protein").

20 The nucleotide sequence of ml243\_1 as presently determined is reported in SEQ ID NO:37, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ml243\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:38. Amino acids 25 to 37 of SEQ ID NO:38 are a predicted leader/signal sequence, with the predicted  
25 mature amino acid sequence beginning at amino acid 38. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ml243\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
30 ml243\_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for ml243\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ml243\_1 demonstrated at least some similarity with sequences

identified as N66656 (yy71a06.s1 Homo sapiens cDNA clone 278962 3'), R17513 (yg02g12.r1 Homo sapiens cDNA clone 31064 5'), Z83837 (Human DNA sequence from Fosmid 113D11 on chromosome 22q11.2-qter contains ESTs, CpG island), and Z84468 (Human DNA sequence from clone 299D3; HTGS phase 1). Based upon sequence  
5 similarity, ml243\_1 proteins and each similar protein or peptide may share at least some activity.

ml243\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 16 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

10

#### Clone "pm96\_9"

A polynucleotide of the present invention has been identified as clone "pm96\_9". pm96\_9 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No.  
15 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pm96\_9 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm96\_9 protein").

The nucleotide sequence of pm96\_9 as presently determined is reported in SEQ  
20 ID NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pm96\_9 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:40.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm96\_9 should be approximately 3600 bp.

25 The nucleotide sequence disclosed herein for pm96\_9 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pm96\_9 demonstrated at least some similarity with sequences identified as AA444024 (zv44d12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 756503 5'), AA488901 (aa55h09.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone  
30 IMAGE:824897 3'), R16408 (yf40b02.r1 Homo sapiens cDNA clone 129291 5'), T19732 (Human gene signature HUMGS00806), U52112 (Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransfer-

ase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28lu2 gene), and Z82250 (Human DNA sequence from cosmid N86D4 on chromosome 22q12-qter contains STS). Based upon sequence similarity, pm96\_9 proteins and each similar protein  
5 or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain at the extreme C-terminus of the pm96\_9 protein sequence (SEQ ID NO:40).

Clone "pu261\_1"

10 A polynucleotide of the present invention has been identified as clone "pu261\_1". pu261\_1 was isolated from a human adult blood (promyelocytic leukemia HL-60) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein.  
15 pu261\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pu261\_1 protein").

The nucleotide sequence of pu261\_1 as presently determined is reported in SEQ ID NO:41, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pu261\_1 protein  
20 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:42. Amino acids 116 to 128 of SEQ ID NO:42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 129. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated  
25 from the remainder of the pu261\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pu261\_1 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for pu261\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
30 FASTA search protocols. pu261\_1 demonstrated at least some similarity with sequences identified as H16093 (ym20g10.r1 Homo sapiens cDNA clone 48582 5'). Based upon sequence similarity, pu261\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential

transmembrane domain within the pu261\_1 protein sequence centered around amino acid 70 of SEQ ID NO:42.

Clone "pw214\_15"

5 A polynucleotide of the present invention has been identified as clone "pw214\_15". pw214\_15 was isolated from a human adult brain (cerebellum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pw214\_15 is a  
10 full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pw214\_15 protein").

The nucleotide sequence of pw214\_15 as presently determined is reported in SEQ ID NO:43, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pw214\_15 protein  
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:44.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pw214\_15 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for pw214\_15 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
20 FASTA search protocols. pw214\_15 demonstrated at least some similarity with sequences identified as AA173391 (zp03a07.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 595284 5'), AA253067 (zr52a10.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 667002 5'), AA523652 ni64d09.s1 NCI\_CGAP\_Pr12 Homo sapiens cDNA clone 981617), and H41832 (yo07b08.r1 Homo sapiens cDNA clone 177207 5'). Based upon  
25 sequence similarity, pw214\_15 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pw214\_15 protein sequence centered around amino acid 15 of SEQ ID NO:44.

30 Clone "qb56\_19"

A polynucleotide of the present invention has been identified as clone "qb56\_19". qb56\_19 was isolated from a human adult bladder (carcinoma 5637) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No.

5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qb56\_19 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qb56\_19 protein").

5       The nucleotide sequence of qb56\_19 as presently determined is reported in SEQ ID NO:45, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qb56\_19 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:46. Amino acids 18 to 40 of SEQ ID NO:46 are a possible leader/signal sequence, with the predicted  
10   mature amino acid sequence beginning at amino acid 41. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the qb56\_19 protein.

      The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
15   qb56\_19 should be approximately 1200 bp.

      The nucleotide sequence disclosed herein for qb56\_19 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qb56\_19 demonstrated at least some similarity with sequences identified as AA632658 (np87c12.s1 NCI\_CGAP\_Thy1 Homo sapiens cDNA clone  
20   IMAGE:1133302), N56430 (JJ8973F Homo sapiens cDNA clone JJ8973 5'), and W05470 (za87f11.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 299565 5'). Based upon sequence similarity, qb56\_19 proteins and each similar protein or peptide may share at least some activity.

      qb56\_19 protein was expressed in a COS cell expression system, and an expressed  
25   protein band of approximately 14 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "qc646\_1"

      A polynucleotide of the present invention has been identified as clone "qc646\_1".  
30   qc646\_1 was isolated from a human adult neural tissue (neuroepithelioma HTB-10 line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded

protein. qc646\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qc646\_1 protein").

The nucleotide sequence of qc646\_1 as presently determined is reported in SEQ ID NO:47, and includes a poly(A) tail. What applicants presently believe to be the proper  
5 reading frame and the predicted amino acid sequence of the qc646\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:48. Amino acids 12 to 24 of SEQ ID NO:48 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 25. Amino acids 32 to 44 are also a predicted leader/signal sequence, with the predicted mature amino acid sequence  
10 beginning at amino acid 45, or are a transmembrane domain. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the qc646\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qc646\_1 should be approximately 1800 bp.

15 The nucleotide sequence disclosed herein for qc646\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qc646\_1 demonstrated at least some similarity with sequences identified as AA470035 (zt94a07.r1 Soares testis NHT Homo sapiens cDNA clone 729972 5'), and AA483957 (ne76e11.s1 NCI\_CGAP\_Ew1 Homo sapiens cDNA clone  
20 IMAGE:910220). The predicted amino acid sequence disclosed herein for qc646\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted qc646\_1 protein demonstrated at least some similarity to sequences identified as D88666 (PS-PLA1 (serine phospholipid-specific phospholipase A) [Rattus norvegicus]), M93284 (lipase related protein 2 [Homo sapiens]),  
25 and R30739 (C-terminally truncated GPL(1-319)), as well as lipases from various other species. Rat PS-PLA1, serine phospholipid-specific phospholipase A, is a member of the lipase family and is secreted from activated platelets. Based upon sequence similarity, qc646\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains  
30 within the qc646\_1 protein sequence, one centered around amino acid 190 and another around amino acid 325 of SEQ ID NO:48. The nucleotide sequence of qc646\_1 indicates that it may contain Alu repetitive elements.

Clone "qf116\_2"

A polynucleotide of the present invention has been identified as clone "qf116\_2". qf116\_2 was isolated from a human adult bladder (carcinoma 5637) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qf116\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qf116\_2 protein").

The nucleotide sequence of qf116\_2 as presently determined is reported in SEQ ID NO:49, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qf116\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:50.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qf116\_2 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for qf116\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qf116\_2 demonstrated at least some similarity with sequences identified as D50810 (placental leucine aminopeptidase [*Homo sapiens*]), R94512 (GTVap (short version), insulin-cleaving aminopeptidase from GLUT-4 vesicles), and U32990 (vp165 [*Rattus norvegicus*]). Human placental leucine aminopeptidase/oxytocinase (P-LAP), a member of the type II membrane-spanning zinc metallopeptidase family, degrades several peptide hormones such as oxytocin and vasopresin, suggesting a role in maintaining homeostasis during pregnancy. The predicted P-LAP amino acid sequence contains the HEXXH consensus sequence of zinc metallopeptidases, indicating that the enzyme belongs to this family, which includes aminopeptidase N and aminopeptidase A. The deduced P-LAP amino acid sequence also contains a hydrophobic region near the N-terminus, suggesting that the enzyme is a type II integral membrane protein. Results suggest that the enzyme is synthesized as an integral membrane protein and is released into blood under some physiological conditions. (See Røgi *et al.*, 1996, *J. Biol. Chem.* **271**(1): 56-61, which is incorporated by reference herein.) Based upon sequence similarity, qf116\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the

qf116\_2 protein sequence, one centered around amino acid 25 and another around amino acid 290 of SEQ ID NO:50.

Clone "qf662\_3"

5 A polynucleotide of the present invention has been identified as clone "qf662\_3". qf662\_3 was isolated from a human adult bladder (carcinoma 5637) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qf662\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to  
10 herein as "qf662\_3 protein").

The nucleotide sequence of qf662\_3 as presently determined is reported in SEQ ID NO:51, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qf662\_3 protein  
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:52. Amino acids 133 to 145 of SEQ ID NO:52 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 146. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated  
20 from the remainder of the qf662\_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qf662\_3 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for qf662\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
25 FASTA search protocols. qf662\_3 demonstrated no significant similarity with sequences in these databases. The nucleotide sequence of qf662\_3 indicates that it may contain repetitive elements.

Clone "am748\_5"

30 A polynucleotide of the present invention has been identified as clone "am748\_5". am748\_5 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. am748\_5 is a full-length



clone, including the entire coding sequence of a secreted protein (also referred to herein as "am748\_5 protein").

The nucleotide sequence of am748\_5 as presently determined is reported in SEQ ID NO:53, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the am748\_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:54. Amino acids 14 to 26 of SEQ ID NO:54 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the am748\_5 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone am748\_5 should be approximately 1550 bp.

The nucleotide sequence disclosed herein for am748\_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. am748\_5 demonstrated at least some similarity with sequences identified as AA418860 (zv98g04.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 767862 5' similar to gb:X14008\_rna1 LYSOZYME C PRECURSOR (HUMAN); contains Alu repetitive element; contains element PTR5 repetitive element), AC003007 (Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence), H73304 (yu27c10.r1 Homo sapiens cDNA clone 235026 5' similar to contains Alu repetitive element), N35175 (yx83d10.r1 Homo sapiens cDNA clone 268339 5' similar to gb X14008\_rna1 LYSOZYME C PRECURSOR (HUMAN); contains Alu repetitive element), N41479 (yy05a11.r1 Homo sapiens cDNA clone 270332 5' similar to gb:X14008\_rna1 LYSOZYME C PRECURSOR (HUMAN)), Q81139 (HPLA2-8 gene), T04964 (EST02852 Homo sapiens cDNA clone HFBCI77), and U18391 (Human Alu sequence clone A8). The predicted amino acid sequence disclosed herein for am748\_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted am748\_5 protein demonstrated at least some similarity to sequences identified as X55777 (put. ORF [Homo sapiens]) and R13556 (Protein encoded downstream of hhc\_M oncoprotein). Based upon sequence similarity, am748\_5 proteins and each similar protein or peptide may share at least some activity. The nucleotide

sequence of am748\_5 indicates that it may contain one or more of the following repetitive elements: Alu, L1.

Clone "cj507\_1"

5 A polynucleotide of the present invention has been identified as clone "cj507\_1".  
cj507\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cj507\_1 is a full-length clone,  
10 including the entire coding sequence of a secreted protein (also referred to herein as "cj507\_1 protein").

The nucleotide sequence of cj507\_1 as presently determined is reported in SEQ ID NO:55, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cj507\_1 protein  
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:56.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cj507\_1 should be approximately 2100 bp.

The nucleotide sequence disclosed herein for cj507\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
20 FASTA search protocols. cj507\_1 demonstrated at least some similarity with sequences identified as AA100356 (zn46a02.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 550442 5' similar to contains element PTR5 repetitive element), AA228100 (zr56g04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667446 3'), AA479997 (zv18b07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753973 5' similar to contains  
25 element PTR5 repetitive element, mRNA sequence), and X85324 (H.sapiens mRNA for non polymorphic CAG repeat (CAG12)). Based upon sequence similarity, cj507\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the cj507\_1 protein sequence centered around amino acid 265 of SEQ ID NO:56. The  
30 nucleotide sequence of cj507\_1 indicates that it may contain a GCA simple repeat region.

cj507\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 47 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "cn922\_5"

A polynucleotide of the present invention has been identified as clone "cn922\_5". cn922\_5 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cn922\_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cn922\_5 protein").

The nucleotide sequence of cn922\_5 as presently determined is reported in SEQ ID NO:57, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cn922\_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:58.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cn922\_5 should be approximately 2200 bp.

The nucleotide sequence disclosed herein for cn922\_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cn922\_5 demonstrated at least some similarity with sequences identified as H34191 (EST110864 Rattus sp. cDNA 5' end), R18707 (yf98f02.r1 Homo sapiens cDNA clone 30546 5'), T26556 (Human gene signature HUMGS08801), and Z83230 (Caenorhabditis elegans cosmid F56A8). The predicted amino acid sequence disclosed herein for cn922\_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cn922\_5 protein demonstrated at least some similarity to sequences identified as AB004535 (HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION [Schizosaccharomyces pombe]) and Z83230 (F56A8.a and F56A8.1 [Caenorhabditis elegans]). Based upon sequence similarity, cn922\_5 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts six potential transmembrane domains within the cn922\_5 protein sequence, centered around amino acids 25, 100, 135, 190, 290, and 370 of SEQ ID NO:58, respectively. The nucleotide sequence of cn922\_5 indicates that it may contain one or more of the following repetitive elements: MER, L1.

Clone "cw691\_11"

A polynucleotide of the present invention has been identified as clone "cw691\_11". cw691\_11 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cw691\_11 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw691\_11 protein").

The nucleotide sequence of cw691\_11 as presently determined is reported in SEQ  
10 ID NO:59, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cw691\_11 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:60.

Another potential cw691\_11 reading frame and predicted amino acid sequence is encoded by basepairs 542 to 970 of SEQ ID NO:59 and is reported in SEQ ID NO:179.  
15 Amino acids 34 to 46 of SEQ ID NO:179 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 47. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:179.

20 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw691\_11 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for cw691\_11 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw691\_11 demonstrated at least some similarity with sequences  
25 identified as AA363712 (EST74158 Pancreas I Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein R10E12.1), AA521201 (aa74c10.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone 826674 3'), AA527142 (ni07a10.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA clone IMAGE 967290, mRNA sequence), AA745501 (ny64d03.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1283045, mRNA sequence), N73108 (yv69a09.r1 Homo sapiens cDNA clone 247960 5'), T19938 (Human gene signature HUMGS01070), and W77963 (zd70d09.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 346001 5' similar to WP:R10E12.1 CE00310).  
30 The predicted amino acid sequence disclosed herein for cw691\_11 was searched against

the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw691\_11 protein demonstrated at least some similarity to sequences identified as P82971 (Bioadhesive precursor protein from cDNA 52), U73679 (YNK1-a [Caenorhabditis elegans]), and Z29561 (R10E12.1 [Caenorhabditis elegans]).

- 5 Based upon sequence similarity, cw691\_11 proteins and each similar protein or peptide may share at least some activity.

#### Clone "cw1000\_2"

- A polynucleotide of the present invention has been identified as clone "cw1000\_2".
- 10 cw1000\_2 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cw1000\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein
- 15 as "cw1000\_2 protein").

- The nucleotide sequence of cw1000\_2 as presently determined is reported in SEQ ID NO:61, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cw1000\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:62. Amino
- 20 acids 24 to 36 of SEQ ID NO:62 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 37. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cw1000\_2 protein.

- 25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw1000\_2 should be approximately 1500 bp.

- The nucleotide sequence disclosed herein for cw1000\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw1000\_2 demonstrated at least some similarity with sequences
- 30 identified as AA446779 (zw89d11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784149 5', mRNA sequence), AA493561 (nh04f07.s1 NCI\_CGAP\_Thy1 Homo sapiens cDNA clone 943333 similar to WP:F15G9.4 CE01552 IG SUPERFAMILY REPEATS ;contains element MSR1 repetitive element), H35690 (EST111696 Rattus sp.

669050: 1190660  
cDNA similar to Opioid binding protein/cell adhesion-like molecule), R18502 (yf96a05.r1  
Homo sapiens cDNA clone 30376 5'), T21582 (Human gene signature HUMGS02965),  
T39504 (ya06g11.r1 Homo sapiens cDNA clone 60740 5'), T46848 (yb94b01.r1 Homo  
sapiens cDNA clone 78793 5'), T51129 (yb94b01.s1 Homo sapiens cDNA clone 78793 3'),  
5 and W67535 (zd40g11.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone  
343172 3' similar to PIR S05539 S05539 glycophorin C - human ;contains element MSR1  
repetitive element). The predicted amino acid sequence disclosed herein for cw1000\_2  
was searched against the GenPept and GeneSeq amino acid sequence databases using the  
BLASTX search protocol. The predicted cw1000\_2 protein demonstrated at least some  
10 similarity to sequences identified as M24406 (poliovirus receptor [Homo sapiens]),  
R07130 (H2OB receptor), W04404 (Human CRTAM; Cytotoxic or Regulatory T-cell  
associated Mol.; CRTAM), X13890 (glycophorin C [Homo sapiens]), and X90569 (elastic  
titin [Homo sapiens]). Based upon sequence similarity, cw1000\_2 proteins and each  
similar protein or peptide may share at least some activity. The TopPredII computer  
15 program predicts an additional potential transmembrane domain within the cw1000\_2  
protein sequence centered around amino acid 358 of SEQ ID NO:62. The nucleotide  
sequence of cw1000\_2 indicates that it may contain a GCC1 repeat element.

20 cw1000\_2 protein was expressed in a COS cell expression system, and an  
expressed protein band of approximately 57 kDa was detected in membrane fractions  
using SDS polyacrylamide gel electrophoresis.

#### Clone "cw1640\_1"

A polynucleotide of the present invention has been identified as clone "cw1640\_1".  
cw1640\_1 was isolated from a human fetal brain cDNA library using methods which are  
25 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
identified as encoding a secreted or transmembrane protein on the basis of computer  
analysis of the amino acid sequence of the encoded protein. cw1640\_1 is a full-length  
clone, including the entire coding sequence of a secreted protein (also referred to herein  
as "cw1640\_1 protein").

30 The nucleotide sequence of cw1640\_1 as presently determined is reported in SEQ  
ID NO:63, and includes a poly(A) tail. What applicants presently believe to be the proper  
reading frame and the predicted amino acid sequence of the cw1640\_1 protein  
corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:64. Amino

acids 123 to 135 of SEQ ID NO:64 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 136. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cw1640\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw1640\_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for cw1640\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw1640\_1 demonstrated at least some similarity with sequences identified as AA075643 (zm88a12.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 544990 5' similar to SW:ACT\_EUPCR P20360 ACTIN), AA411334 (zv29e11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755084 5' similar to WP:C49H3.8 CE04234 ACTIN-LIKE PROTEIN ), AA913364 (ol37b07.s1 Soares NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1525621 3' similar to WP:C49H3.8 CE04234 ACTIN-LIKE PROTEIN, mRNA sequence), N25416 (yx40g10.r1 Homo sapiens cDNA clone 264258 5' similar to SP ACT2\_PLAFA P14883 ACTIN), R96887 (yq61g10.r1 Homo sapiens cDNA clone 200322 5'), W37097 (zb98h03.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320885 5'), W44778 (zb98h03.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320885 3'), W61038 (zc54g09.r1 Soares senescent fibroblasts NbHSF Homo), W76570 (zd66f12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 345647 5' similar to SW:ACT\_PROCL P45521 ACTIN), and W82519 (mf05b01.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone). The predicted amino acid sequence disclosed herein for cw1640\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw1640\_1 protein demonstrated at least some similarity to sequences identified as J00068 (alpha-actin [Homo sapiens]), J01163 (actin [Oxytricha fallax]), R22026 (A. chrysogenum actin), R50328 (Drug resistant structural protein), U42436 (Similar to actin-like protein [Caenorhabditis elegans]), and U90439 (actin isolog [Arabidopsis thaliana]). Based upon sequence similarity, cw1640\_1 proteins and each similar protein or peptide may share at least some activity.

Clone "d24\_1"

A polynucleotide of the present invention has been identified as clone "d24\_1". A cDNA clone was first isolated from a human adult blood (peripheral blood mononuclear cells treated with concanavalin A and phorbol myristate acetate) cDNA library using  
5 methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate d24\_1 from a human adult blood (peripheral blood mononuclear cells treated with phytohemagglutinin, phorbol myristate acetate, and mixed lymphocyte  
10 reaction) cDNA library. d24\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "d24\_1 protein").

The nucleotide sequence of d24\_1 as presently determined is reported in SEQ ID NO:65, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the d24\_1 protein corresponding  
15 to the foregoing nucleotide sequence is reported in SEQ ID NO:66. Amino acids 124 to 136 of SEQ ID NO:66 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 137. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the d24\_1  
20 protein. The mRNA sequence encoding amino acids 172 to 175 of SEQ ID NO:66 may not be present in alternatively-spliced forms of d24\_1 mRNA molecules.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone d24\_1 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for d24\_1 was searched against the  
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. d24\_1 demonstrated at least some similarity with sequences identified as AA478740 (zv14g12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 753670 3'), AA479444 (zv14g12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753670 5', mRNA sequence), AA278581 (zs76f09.r1 Soares NbHTGBC Homo sapiens  
30 cDNA clone 703433 5' similar to WP T04A8.12 CE01067 YEAST 107.9KD PGK1-MAK32 INTERGENIC HYPOTHETICAL PROTEIN), H05202 (yl85h02.r1 Homo sapiens cDNA clone 45213 5' similar to SP T04A8.12m CE01067 YEAST 107.9KD PGK1-MAK32 INTERGENIC HYPOTHETICAL PROTEIN), R74287 (yi57e07.r1 Homo



5 sapiens cDNA clone 143364 5'), U57715 (*Rattus norvegicus* FGF receptor activating protein FRAG1 (FRAG1) mRNA, complete CDs), and Z35663 (*C. elegans* protein of unknown function). The predicted amino acid sequence disclosed herein for d24\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted d24\_1 protein demonstrated at least some similarity to the sequence identified as U57715 (FGF receptor activating protein FRAG1 [*Rattus norvegicus*]). Lorenzi *et al.* (1996, *Proc. Natl. Acad. Sci. USA* 93:8956, incorporated by reference herein) studied the FRAG1 gene in rat osteosarcoma cells. They concluded that the FRAG1 gene product gets fused to FGF receptor 2 (FGFR2). This fusion "drastically stimulates the transforming activity and autophosphorylation of the receptor" and causes oncogenicity. Based upon sequence similarity, d24\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the d24\_1 protein sequence, centered around amino acids 34, 154, and 194 of SEQ ID NO:66, respectively.

d24\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 24 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### 20 Clone "dd426\_1"

A polynucleotide of the present invention has been identified as clone "dd426\_1". A cDNA clone was first isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate dd426\_1 from a human adult testes (teratocarcinoma NCCIT) cDNA library. dd426\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dd426\_1 protein").

The nucleotide sequence of dd426\_1 as presently determined is reported in SEQ ID NO:67, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dd426\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:68. Amino acids 76 to 88 of SEQ ID NO:68 are a predicted leader/signal sequence, with the predicted

669050-1190650  
mature amino acid sequence beginning at amino acid 89. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the dd426\_1 protein.

5           The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dd426\_1 should be approximately 800 bp.

          The nucleotide sequence disclosed herein for dd426\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dd426\_1 demonstrated at least some similarity with sequences  
10 identified as AA760716 (nz13d06.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1287659 similar to WP:F13H10.3 CE05624 YEAST YEH4 LIKE PROTEIN; mRNA sequence), H11919 (ym10e10.r1 Homo sapiens cDNA clone 47462 5'), and Z68748 (Caenorhabditis elegans cosmid F13H10). The predicted amino acid sequence disclosed herein for dd426\_1 was searched against the GenPept and GeneSeq amino acid  
15 sequence databases using the BLASTX search protocol. The predicted dd426\_1 protein demonstrated at least some similarity to sequences identified as U39782 (lysine and histidine specific transporter [Arabidopsis thaliana]) and Z68748 (F13H10.3 [Caenorhabditis elegans]). Based upon sequence similarity, dd426\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program  
20 predicts an additional potential transmembrane domain within the dd426\_1 protein sequence centered around amino acid 30 of SEQ ID NO:68, which may also function as a leader/signal sequence.

          dd426\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 12 kDa was detected in membrane fractions using SDS  
25 polyacrylamide gel electrophoresis.

#### Clone "di393\_2"

          A polynucleotide of the present invention has been identified as clone "di393\_2". di393\_2 was isolated from a human adult testes cDNA library using methods which are  
30 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. di393\_2 is a full-length clone,

including the entire coding sequence of a secreted protein (also referred to herein as "di393\_2 protein").

The nucleotide sequence of di393\_2 as presently determined is reported in SEQ ID NO:69, and includes a poly(A) tail. What applicants presently believe to be the proper  
5 reading frame and the predicted amino acid sequence of the di393\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:70. Amino acids 7 to 19 of SEQ ID NO:70 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain  
10 should the predicted leader/signal sequence not be separated from the remainder of the di393\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone di393\_2 should be approximately 600 bp.

The nucleotide sequence disclosed herein for di393\_2 was searched against the  
15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. di393\_2 demonstrated at least some similarity with sequences identified as AA669506 (zu85g08.s1 Soares testis NHT Homo sapiens cDNA clone 744830 3', mRNA sequence). Based upon sequence similarity, di393\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer  
20 program predicts an additional potential transmembrane domain within the di393\_2 protein sequence centered around amino acid 66 of SEQ ID NO:70.

di393\_2 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 20 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

25

#### Clone "dj167\_2"

A polynucleotide of the present invention has been identified as clone "dj167\_2". dj167\_2 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
30 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dj167\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dj167\_2 protein").

The nucleotide sequence of dj167\_2 as presently determined is reported in SEQ ID NO:71, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dj167\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:72.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dj167\_2 should be approximately 1550 bp.

The nucleotide sequence disclosed herein for dj167\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dj167\_2 demonstrated at least some similarity with sequences  
10 identified as H49161 (yq18d05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 274208 5'), L12350 (Human thrombospondin 2 (THBS2) mRNA, complete cds), T98917 (ye66b03.s1 Homo sapiens cDNA clone 122669 3' similar to SP:TSP1\_CHICK P35440 THROMBOSPONDIN 1), and X87620 (B.taurus mRNA for complete thrombospondin). The predicted amino acid sequence disclosed herein for dj167\_2 was  
15 searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dj167\_2 protein demonstrated at least some similarity to sequences identified as L12350 (thrombospondin 2 [Homo sapiens]), M60853 (thrombospondin [Gallus gallus]), R40823 (Human thrombospondin 1), U48245 (protein kinase C-binding protein Nel [Rattus norvegicus]), X87620 (thrombospondin [Bos  
20 taurus]), and Z71178 (B0024.14 [Caenorhabditis elegans]). Based upon sequence similarity, dj167\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the dj167\_2 protein sequence, centered around amino acids 140, 215, and 315 of SEQ ID NO:72, respectively.

25

#### Clone "dj167\_19"

A polynucleotide of the present invention has been identified as clone "dj167\_19". dj167\_19 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
30 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dj167\_19 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dj167\_19 protein").

669050 "TTTGGG50"

The nucleotide sequence of dj167\_19 as presently determined is reported in SEQ ID NO:73, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dj167\_19 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:74. Amino acids 22 to 34 of SEQ ID NO:74 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 35. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the dj167\_19 protein. The dj167\_19 clone is related to that of dj167\_2, and extends further 5'. The dj167\_19 clone appears to contain coding sequences for chorionic somatomammotropin in the opposite orientation at its 5' end between Sfi restriction sites (at nucleotides 16 and 839 of SEQ ID NO:73). The dj167\_2 and dj167\_19 clones may represent alternatively spliced messenger RNA molecules encoding two different forms of a secreted protein.

15 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dj167\_19 should be approximately 4500 bp.

Analysis of the dj167\_19 amino acid sequence (SEQ ID NO:74) reveals the following domains: IGFBP cysteine-rich domain at amino acids 60-75; VWF-B cysteine-rich domains at amino acids 174-210, 212-247, 255-291, and 293-328; Chordin cysteine-rich domains at amino acids 336-390, 403-456, 608-662, 679-734, 753-808, and 819-873; Antistatin (protease inhibitor) cysteine-rich domains at amino acids 469-498, 505-532, 539-564, and 567-592; RGD cell attachment sequence at amino acids 314-316, and Asn glycosylation sites at amino acids 71, 113, 330, 474, and 746. The cysteine-rich domains listed above are similar to domains found in the C domain of Von Willebrand Factor (VWF), and in procollagen and thrombospondin. In addition, the amino acid sequence of SEQ ID NO:74 from amino acid 938 to amino acid 960 appears to be a transmembrane domain.

25 The dj167\_19 transcript is expressed in several cell types, including kidney, pancreas, spleen, and ovary, and is most abundantly expressed in placental tissue.

30

#### Clone "dw665\_4"

A polynucleotide of the present invention has been identified as clone "dw665\_4". dw665\_4 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was

identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dw665\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dw665\_4 protein").

5           The nucleotide sequence of dw665\_4 as presently determined is reported in SEQ ID NO:75, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dw665\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:76. Amino acids 15 to 27 of SEQ ID NO:76 are a predicted leader/signal sequence, with the predicted  
10   mature amino acid sequence beginning at amino acid 28. Amino acids 16 to 28 of SEQ ID NO:76 are also a predicted leader/signal sequence, with the predicted mature amino acid sequence in that case beginning at amino acid 29. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the dw665\_4 protein.

15           The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dw665\_4 should be approximately 3750 bp.

          The nucleotide sequence disclosed herein for dw665\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dw665\_4 demonstrated at least some similarity with sequences  
20   identified as AA029053 (zk09f06.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 470051 3'), H77289 (EST27o17 WATM1 Homo sapiens cDNA clone 27o17, mRNA sequence), and T21722 (Human gene signature HUMGS03170). The predicted amino acid sequence disclosed herein for dw665\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted  
25   dw665\_4 protein demonstrated at least some similarity to sequences identified as L35764 (chordin [*Xenopus laevis*]) and W31559 (*Xenopus* frog protein "chordin"). Analysis of motifs within the predicted dw665\_4 protein revealed the presence of Chordin cysteine-rich domains at amino acids 37-99, 115-178, and 260-322 of SEQ ID NO:76; an 'RGD' cell-attachment sequence (at amino acids 179-181 of SEQ ID NO:76), which in some  
30   proteins has been shown to play a role in cell adhesion; and Asp glycosylation sites at amino acids 118 and 291. Based upon sequence similarity, dw665\_4 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of dw665\_4 indicates that it may contain an AC repetitive element.

dw665\_4 transcripts are expressed in many tissues including kidney, adrenal gland, and prostate tissues, and are most abundantly expressed in pancreas; however, little or no dw665\_4 transcript expression is observed in liver or peripheral blood cells. dw665\_4 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 75 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis; two additional bands at approximately 26 and 30 kDa were also observed. BIACORE binding experiments indicate that dw665\_4 protein has a Chordin-like protein-binding profile, and binds to BMP-2, BMP-4, BMP-7, BMP-12, and GDF-5.

#### Clone "dx146\_12"

A polynucleotide of the present invention has been identified as clone "dx146\_12". dx146\_12 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dx146\_12 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dx146\_12 protein").

The nucleotide sequence of dx146\_12 as presently determined is reported in SEQ ID NO:77, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dx146\_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:78.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dx146\_12 should be approximately 2250 bp.

The nucleotide sequence disclosed herein for dx146\_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dx146\_12 demonstrated at least some similarity with sequences identified as AA090429 (y0527.seq.F Fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'), AA232068 (zr24a01.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 664296 5'), AA886679 (oj47h07.s1 NCI\_CGAP\_Kid3 Homo sapiens cDNA clone IMAGE:1501501 3' similar to WP:F16A11.2 CE09424 METHANOCOCCUS HYPOTHETICAL PROTEIN 0682 LIKE; mRNA sequence), R61436 (yh15g06.r1 Homo sapiens cDNA clone 37884 5'), and Z81505 (Caenorhabditis elegans

cosmid F16A11, complete sequence). The predicted amino acid sequence disclosed herein for dx146\_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dx146\_12 protein demonstrated at least some similarity to sequences identified as U67515 (hypothetical protein (SP P46850) [Methanococcus jannaschii]) and Z81505 (F16A11.2 [Caenorhabditis elegans]). Based upon sequence similarity, dx146\_12 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the dx146\_12 protein sequence centered around amino acid 405 of SEQ ID NO:78.

dx146\_12 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 50 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "dx219\_13"

A polynucleotide of the present invention has been identified as clone "dx219\_13". dx219\_13 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dx219\_13 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dx219\_13 protein").

The nucleotide sequence of dx219\_13 as presently determined is reported in SEQ ID NO:79, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dx219\_13 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:80. Amino acids 94 to 106 of SEQ ID NO:80 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 107. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the dx219\_13 protein.



The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dx219\_13 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for dx219\_13 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dx219\_13 demonstrated at least some similarity with sequences identified as AA429731 (zw66g05.s1 Soares testis NHT Homo sapiens cDNA clone 781208 3'), AA446067 (zw66e06.r1 Soares testis NHT Homo sapiens cDNA clone 781186 5', mRNA sequence), T23212 (standard; cDNA to mRNA; 161 BP, Human gene signature HUMGS05005), W29299 (mb99f03.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone 337565 5'), W87852 (zh68b05.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 417201 5'), and Y13897 (Homo sapiens partial mRNA for hypothetical protein). Based upon sequence similarity, dx219\_13 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the dx219\_13 protein sequence, one centered around amino acid 160 and another around amino acid 275 of SEQ ID NO:80.

dx219\_13 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 37 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "fm3\_1"

A polynucleotide of the present invention has been identified as clone "fm3\_1". fm3\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fm3\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "fm3\_1 protein").

The nucleotide sequence of fm3\_1 as presently determined is reported in SEQ ID NO:81, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the fm3\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:82. Amino acids 7 to 19 of SEQ ID NO:82 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the

predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the fm3\_1 protein.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fm3\_1 should be approximately 600 bp.

The nucleotide sequence disclosed herein for fm3\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fm3\_1 demonstrated at least some similarity with sequences identified as T15669 (IB1718 Infant brain, Bento Soares Homo sapiens cDNA 3'end).  
10 Based upon sequence similarity, fm3\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domains within the fm3\_1 protein sequence centered around amino acid 85 of SEQ ID NO:82.

fm3\_1 protein was expressed in a COS cell expression system, and an expressed  
15 protein band of approximately 9 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "h225\_1"

A polynucleotide of the present invention has been identified as clone "h225\_1".  
20 h225\_1 was isolated from a human adult blood (peripheral blood mononuclear cells treated with phytohemagglutinin and phorbol myristate acetate and mixed lymphocyte reaction) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of  
25 the encoded protein. h225\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "h225\_1 protein").

The nucleotide sequence of h225\_1 as presently determined is reported in SEQ ID NO:83. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the h225\_1 protein corresponding to the foregoing  
30 nucleotide sequence is reported in SEQ ID NO:84. Amino acids 52 to 64 of SEQ ID NO:84 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 65. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the h225\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone h225\_1 should be approximately 832 bp.

The nucleotide sequence disclosed herein for h225\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. h225\_1 demonstrated at least some similarity with sequences identified as AA604374 (no87e01.s1 NCI\_CGAP\_AA1 Homo sapiens cDNA clone IMAGE:1113816 similar to WP:ZK757.1 CE00467; mRNA sequence), H18393 (yn49a12.r1 Homo sapiens cDNA clone 171742 5' similar to SP:ZK757.1 CE00467), and R23642 (yh35e03.r1 Homo sapiens cDNA clone 131740 5'). The predicted amino acid sequence disclosed herein for h225\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted h225\_1 protein demonstrated at least some similarity to sequences identified as AL022600 (hypothetical protein [Schizosaccharomyces pombe]) and Z48758 (SC9727\_21 unknown [Saccharomyces cerevisiae]). Based upon sequence similarity, h225\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "kj320\_1"

A polynucleotide of the present invention has been identified as clone "kj320\_1". kj320\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. kj320\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "kj320\_1 protein").

The nucleotide sequence of kj320\_1 as presently determined is reported in SEQ ID NO:85, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the kj320\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:86. Amino acids 26 to 38 of SEQ ID NO:86 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 39. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the kj320\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone kj320\_1 should be approximately 4900 bp.

The nucleotide sequence disclosed herein for kj320\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. kj320\_1 demonstrated at least some similarity with sequences identified as A45343 (Sequence 13 from Patent WO9517522), AA284111 (zc36f08.T7 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324423 3' similar to WP ZK688.8 CE00544 UDP-GALNAC; mRNA sequence), AA375707 (EST88026 HSC172 cells II Homo sapiens cDNA 5' end), AA534406 (nf76b08.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE 925815), D39885 (Rice cDNA, partial sequence (S1531\_1A)), G10010 (human STS CHLC.GCT16E06.P18287 clone GCT16E06), Q75104 (Cattle GalNAc-transferase), Q95187 (Simple tandem repeat (STR) corresponding to wg1d10), and U35890 (Rattus norvegicus polypeptide GalNAc transferase T1 mRNA, complete cds). The predicted amino acid sequence disclosed herein for kj320\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted kj320\_1 protein demonstrated at least some similarity to sequences identified as R66397 (Cattle GalNAc-transferase), U41514 (UDP-GalNAc polypeptide N-acetylgalactosaminyltransferase [Homo sapiens]), and X85018 (UDP-GalNAc polypeptide N-acetylgalactosaminyl transferase [Homo sapiens]). Analysis of motifs within kj320\_1 reveals the presence of the alpha-2-macroglobulin family thiolester region signature. The proteinase-binding alpha-macroglobulins (A2M) are large glycoproteins found in the plasma of vertebrates, in the hemolymph of some invertebrates, and in reptilian and avian egg white. They inhibit all four classes of proteinases by trapping a proteinase with a peptide stretch containing the specific cleavage site (the 'bait' region) which upon proteinase binding induces a conformational change in the protein, trapping the proteinase. Upon cleavage of the 'bait' region, a covalent bond (a thiol-ester bond between the side chains of a cysteine and a glutamine) is formed between the A2M and the proteinase. Based upon sequence similarity, kj320\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of kj320\_1 indicates that it may contain one or more repetitive elements.

kj320\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 136 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

5        Clone "ml236\_5"

A polynucleotide of the present invention has been identified as clone "ml236\_5". ml236\_5 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer  
10      analysis of the amino acid sequence of the encoded protein. ml236\_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ml236\_5 protein").

The nucleotide sequence of ml236\_5 as presently determined is reported in SEQ ID NO:87, and includes a poly(A) tail. What applicants presently believe to be the proper  
15      reading frame and the predicted amino acid sequence of the ml236\_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:88. Amino acids 148 to 160 of SEQ ID NO:88 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 161. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a  
20      transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ml236\_5 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ml236\_5 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for ml236\_5 was searched against the  
25      GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ml236\_5 demonstrated at least some similarity with sequences identified as AA137204 (zl23h11.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 502821 3'), AA307966 (EST17887 Aorta endothelial cells, TNF alpha-treated Homo sapiens cDNA 5' end, mRNA sequence), AA434504 (zw31c03.r1 Soares ovary tumor  
30      NbHOT Homo sapiens cDNA clone 770884 5' similar to WP C45G9.7 CE01858), AA525971 (ni93g09.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA clone 984448), AA526490 (ni96c11.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA clone IMAGE 984692, mRNA sequence), AF028823 (Homo sapiens Tax interaction protein 1 mRNA, partial

cds), U90913 (Human clone 23665 mRNA sequence), and W73114 (zd55c12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344566 5'). The predicted amino acid sequence disclosed herein for ml236\_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted  
5 ml236\_5 protein demonstrated at least some similarity to sequences identified as AF028823 (Tax interaction protein 1 [Homo sapiens]) and U21323 (similar to tight junction protein (ZO-1) (SP Z01\_HUMAN, Q07157) [Caenorhabditis elegans]). Based upon sequence similarity, ml236\_5 proteins and each similar protein or peptide may share at least some activity.

10 ml236\_5 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 14 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "pu282\_10"

15 A polynucleotide of the present invention has been identified as clone "pu282\_10". pu282\_10 was isolated from a human adult blood (promyelocytic leukemia HL-60) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein.  
20 pu282\_10 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pu282\_10 protein").

The nucleotide sequence of pu282\_10 as presently determined is reported in SEQ ID NO:89, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pu282\_10 protein  
25 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:90. Amino acids 119 to 131 of SEQ ID NO:90 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 132. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated  
30 from the remainder of the pu282\_10 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pu282\_10 should be approximately 1050 bp.

5 The nucleotide sequence disclosed herein for pu282\_10 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pu282\_10 demonstrated at least some similarity with sequences identified as AA311503 (EST182442 Jurkat T-cells VI Homo sapiens cDNA 5' end),  
10 AA336709 (EST41341 Endometrial tumor Homo sapiens cDNA 5' end), AA336890 (EST41572 Endometrial tumor), AA385588 (EST99290 Thyroid Homo sapiens cDNA 5' end), AA526889 (ni09e05.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA clone IMAGE:967520), AC003058 (Arabidopsis thaliana "unknown" protein), and T19726 (Human gene signature HUMGS00800). Based upon sequence similarity, pu282\_10 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the pu282\_10 protein sequence, one centered around amino acid 39 and another around amino acid 95 of SEQ ID NO:90.

15 pu282\_10 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 16 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "at94\_2"

20 A polynucleotide of the present invention has been identified as clone "at94\_2". at94\_2 was isolated from a human adult blood (lymphocytes and dendritic cells treated with mixed lymphocyte reaction) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. at94\_2 is a full-length clone, including the  
25 entire coding sequence of a secreted protein (also referred to herein as "at94\_2 protein").

The nucleotide sequence of at94\_2 as presently determined is reported in SEQ ID NO:91, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the at94\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:92. Amino acids 214 to  
30 226 of SEQ ID NO:92 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 227. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should

the predicted leader/signal sequence not be separated from the remainder of the at94\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone at94\_2 should be approximately 4300 bp.

5        The nucleotide sequence disclosed herein for at94\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. at94\_2 demonstrated at least some similarity with sequences identified as N24317 (yx23d12.r1 Homo sapiens cDNA clone 262583 5'), T30988 (EST25695 Homo sapiens cDNA 5' end similar to None), and U37026 (Rattus norvegicus  
10 brain sodium channel beta 2 subunit (SCNB2) mRNA, complete cds). The predicted amino acid sequence disclosed herein for at94\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted at94\_2 protein demonstrated at least some similarity to the sequence identified as Z49912 (T24F1.2 [Caenorhabditis elegans]). Based upon sequence similarity, at94\_2 proteins and  
15 each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four additional potential transmembrane domains within the at94\_2 protein sequence, centered around amino acids 23, 306, 332, and 364 of SEQ ID NO:92, respectively.

20        Clone "bf169\_13"

A polynucleotide of the present invention has been identified as clone "bf169\_13". bf169\_13 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer  
25 analysis of the amino acid sequence of the encoded protein. bf169\_13 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bf169\_13 protein").

The nucleotide sequence of bf169\_13 as presently determined is reported in SEQ ID NO:93, and includes a poly(A) tail. What applicants presently believe to be the proper  
30 reading frame and the predicted amino acid sequence of the bf169\_13 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:94. Amino acids 342 to 354 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 355. Due to the hydrophobic nature of this



possible leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the bf169\_13 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bf169\_13 should be approximately 3000 bp.

5        The nucleotide sequence disclosed herein for bf169\_13 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bf169\_13 demonstrated at least some similarity with sequences identified as AA227952 (zr56b06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667379 3'), AA453914 (zx32e11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA  
10    clone 788204 5' similar to contains element TAR1 repetitive element; mRNA sequence), H46157 (yo13f11.r1 Homo sapiens cDNA clone 177837 5'), H18792 (yn52e02.r1 Homo sapiens cDNA clone 172058 5'), and N24601 (yx72e01.s1 Homo sapiens cDNA clone 267288 3'). The predicted amino acid sequence disclosed herein for bf169\_13 was searched against the GenPept and GeneSeq amino acid sequence databases using the  
15    BLASTX search protocol. The predicted bf169\_13 protein demonstrated at least some similarity to sequences identified as L41834 (plant nuclear protein [Ensis minor]) and Z75539 (F28C1.1 [Caenorhabditis elegans]). Analysis of motifs in the predicted bf169\_13 protein revealed a "mitochondrial energy transfer proteins" signature at amino acid 574 of SEQ ID NO:94. Based upon sequence similarity, bf169\_13 proteins and each similar  
20    protein or peptide may share at least some activity. The nucleotide sequence of bf169\_13 indicates that it may contain one or more GCCCCA, GCCC, GGA and/or GC repeat sequences.

bf169\_13 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 109 kDa was detected in membrane fractions  
25    using SDS polyacrylamide gel electrophoresis.

#### Clone "bl152\_12"

A polynucleotide of the present invention has been identified as clone "bl152\_12". bl152\_12 was isolated from a human adult testes cDNA library using methods which are  
30    selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bl152\_12 is a full-length

clone, including the entire coding sequence of a secreted protein (also referred to herein as "bl152\_12 protein").

The nucleotide sequence of bl152\_12 as presently determined is reported in SEQ ID NO:95, and includes a poly(A) tail. What applicants presently believe to be the proper  
5 reading frame and the predicted amino acid sequence of the bl152\_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:96.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bl152\_12 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for bl152\_12 was searched against the  
10 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bl152\_12 demonstrated at least some similarity with sequences identified as AA280876 (zs97d04.s1 NCI\_CGAP\_GCB1 Soares NbHTGBC Homo sapiens cDNA clone 711559 3' similar to contains element MER22 repetitive element), AA280956 (zs97d04.r1 NCI\_CGAP\_GCB1 Soares NbHTGBC Homo sapiens cDNA clone 711559  
15 5'), R21512 (yh19b03.s1 Homo sapiens cDNA clone 130157 3'), R67018 (yi26e05.s1 Homo sapiens cDNA clone 140384 3' similar to contains MER22 repetitive element), R71877 (yj87d11.s1 Homo sapiens cDNA clone 155733 3' similar to contains MER22 repetitive element), T22941 (Human gene signature HUMGS04666), W46539 (zc30g03.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 323860 3', mRNA  
20 sequence), and W70065 (zd49c04.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone). The predicted amino acid sequence disclosed herein for bl152\_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bl152\_12 protein demonstrated at least some similarity to the sequence identified as Z82256 (B0513.2 [Caenorhabditis elegans]). Based upon  
25 sequence similarity, bl152\_12 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of bl152\_12 indicates that it may contain one or more GCC repeat sequences.

bl152\_12 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 25 kDa was detected in conditioned medium using SDS  
30 polyacrylamide gel electrophoresis.

Clone "bz578\_1"

A polynucleotide of the present invention has been identified as clone "bz578\_1". bz578\_1 was isolated from a human fetal kidney cDNA library using methods and was identified as encoding a novel protein on the basis of computer analysis of the amino acid  
5 sequence of the encoded protein. bz578\_1 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "bz578\_1 protein").

The nucleotide sequence of bz578\_1 as presently determined is reported in SEQ ID NO:97, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bz578\_1 protein  
10 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:98.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bz578\_1 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for bz578\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
15 FASTA search protocols. bz578\_1 demonstrated at least some similarity with sequences identified as T47038 (yb12e08.r1 Homo sapiens cDNA clone 70982 5' contains L1 repetitive element) and Z82975 (Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X). The predicted amino acid sequence disclosed herein for bz578\_1 was searched against the GenPept and GeneSeq amino acid sequence  
20 databases using the BLASTX search protocol. The predicted bz578\_1 protein demonstrated at least some similarity to sequences identified as AF051782 (diaphanous 1 [Homo sapiens]), U96963 (diaphanous 1 [mouse]), and U93572 (putative p150 [Homo sapiens]). Based upon sequence similarity, bz578\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of bz578\_1 indicates  
25 that it may contain one or more L1 repeat sequences.

Clone "cb123\_1"

A polynucleotide of the present invention has been identified as clone "cb123\_1". cb123\_1 was isolated from a human fetal brain cDNA library using methods which are  
30 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cb123\_1 is a full-length clone,

including the entire coding sequence of a secreted protein (also referred to herein as "cb123\_1 protein").

The nucleotide sequence of cb123\_1 as presently determined is reported in SEQ ID NO:99, and includes a poly(A) tail. What applicants presently believe to be the proper  
5 reading frame and the predicted amino acid sequence of the cb123\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:100. Amino acids 44 to 56 of SEQ ID NO:100 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 57. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a  
10 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cb123\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cb123\_1 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for cb123\_1 was searched against the  
15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cb123\_1 demonstrated at least some similarity with sequences identified as AA309020 (EST179803 Colon carcinoma (Caco-2) cell line I Homo sapiens cDNA 5' end, mRNA sequence), R89617 (ym98b08.s1 Homo sapiens cDNA clone 166935 3'), T16814 (NIB1893 Normalized infant brain, Bento Soares Homo sapiens cDNA 3'end  
20 similar to EST02882 H. sapiens cDNA clone HFBCL71), T24092 (Human gene signature HUMGS06080), and T55187 (yb43e06.s1 Homo sapiens cDNA clone 73954 3'). The predicted amino acid sequence disclosed herein for cb123\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cb123\_1 protein demonstrated at least some similarity to the sequence  
25 identified as U33331 (orf UL133 [Human cytomegalovirus]). Based upon sequence similarity, cb123\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the cb123\_1 protein sequence, one centered around amino acid 15 and another around amino acid 80 of SEQ ID NO:100.

30

#### Clone "ch245\_1"

A polynucleotide of the present invention has been identified as clone "ch245\_1". ch245\_1 was isolated from a human fetal kidney cDNA library using methods which are

selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ch245\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ch245\_1 protein").

The nucleotide sequence of ch245\_1 as presently determined is reported in SEQ ID NO:101, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ch245\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:102. The TopPredII computer program predicts a potential transmembrane domain within the ch245\_1 protein sequence centered around amino acid 87 of SEQ ID NO:102.

Another potential ch245\_1 reading frame and predicted amino acid sequence is encoded by basepairs 533 to 778 of SEQ ID NO:101 and is reported in SEQ ID NO:180. The TopPredII computer program predicts a potential transmembrane domain within the SEQ ID NO:180 amino acid sequence centered around amino acid 34 of SEQ ID NO:180.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ch245\_1 should be approximately 1350 bp.

The nucleotide sequence disclosed herein for ch245\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ch245\_1 demonstrated at least some similarity with sequences identified as AA402307 (zu48f03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 741245 5', mRNA sequence), H19032 (ym44e04.r1 Homo sapiens cDNA clone 50921 5'), H19323 (ym44e04.s1 Homo sapiens cDNA clone 50921 3'), and N36070 (yy02g11.r1 Homo sapiens cDNA clone 270116 5'). The predicted amino acid sequence disclosed herein for ch245\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ch245\_1 protein demonstrated at least some similarity to the sequence identified as M58597 (ELAM-1 ligand fucosyltransferase [Homo sapiens]) and U36763 (fatty acid synthase [Mycobacterium bovis]). Based upon sequence similarity, ch245\_1 proteins and each similar protein or peptide may share at least some activity.

Clone "cj378\_3"

A polynucleotide of the present invention has been identified as clone "cj378\_3". cj378\_3 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cj378\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cj378\_3 protein").

The nucleotide sequence of cj378\_3 as presently determined is reported in SEQ ID  
10 NO:103, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cj378\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:104.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cj378\_3 should be approximately 1400 bp.

15 The nucleotide sequence disclosed herein for cj378\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cj378\_3 demonstrated at least some similarity with sequences identified as D60138 (Human fetal brain cDNA 5'-end GEN-088A04, mRNA sequence), H19318 (ym44d06.s1 Homo sapiens cDNA clone 51231 3'), H41859 (yo07g06.r1 Homo  
20 sapiens cDNA clone 177274 5'), T25386 (Human gene signature HUMGS07551), and T75383 (yc89g05.r1 Homo sapiens cDNA clone 23351 5'). Based upon sequence similarity, cj378\_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain at the N-terminus of the the cj378\_3 protein sequence (SEQ ID NO:104).

25

Clone "cw1481\_1"

A polynucleotide of the present invention has been identified as clone "cw1481\_1". cw1481\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
30 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cw1481\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw1481\_1 protein").

The nucleotide sequence of cw1481\_1 as presently determined is reported in SEQ ID NO:105, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cw1481\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:106.

5           The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw1481\_1 should be approximately 2380 bp.

          The nucleotide sequence disclosed herein for cw1481\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw1481\_1 demonstrated at least some similarity with sequences  
10 identified as AA027927 (zk05a10.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469626 5'), AA027928 (zk05a10.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469626 3' similar to contains MER28.b2 MER28 repetitive element), AA113357 (zn69g06.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 563482 3'), AA252304 (zs12b08.s1 Soares NbHTGBC Homo sapiens cDNA clone 684951  
15 3' similar to contains element MER22 repetitive element), AA976744 (oq09a09.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA clone IMAGE 1585816 3' similar to TR O15025 O15025 KIAA0308 ;contains element MER22 repetitive element; mRNA sequence), R55084 (yg87a06.r1 Homo sapiens cDNA clone 40244 5'), U00930 (Human clone C4E 1.63 (CAC)n/(GTG)n repeat-containing mRNA), U00955 (Human clone CE29 8.1  
20 (CAC)n/(GTG)n repeat-containing mRNA), and W16808 (zb93a09.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320344 3'). The predicted amino acid sequence disclosed herein for cw1481\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw1481\_1 protein demonstrated at least some similarity to sequences identified as AB002306 (KIAA0308  
25 [Homo sapiens]), X15906 (precursor polypeptide), and Z68751 (F01G4.1 [Caenorhabditis elegans]). Based upon sequence similarity, cw1481\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the cw1481\_1 protein sequence centered around amino acid 431 of SEQ ID NO:106, and a putative transmembrane domain within the  
30 cw1481\_1 protein sequence centered around amino acid 395 of SEQ ID NO:106. The amino acid sequence of cw1481\_1 indicates that it has a histidine-rich region and a serine-rich region, and it is strongly internally repeated.

Clone "dd119\_4"

A polynucleotide of the present invention has been identified as clone "dd119\_4". dd119\_4 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dd119\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dd119\_4 protein").

The nucleotide sequence of dd119\_4 as presently determined is reported in SEQ  
10 ID NO:107, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dd119\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:108. Amino acids 27 to 39 of SEQ ID NO:108 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 40. Due to the  
15 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the dd119\_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dd119\_4 should be approximately 3350 bp.

20 The nucleotide sequence disclosed herein for dd119\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dd119\_4 demonstrated at least some similarity with sequences identified as AA151924 (zo30e05.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 588416 5' similar to SW SLIT\_DROME P24014 SLIT PROTEIN PRECURSOR;  
25 mRNA sequence), AA193464 (zr41c06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 665962 3'), AB011135 (Homo sapiens mRNA for KIAA0563 protein, complete cds), G23888 (human STS WI-12393), H04996 (yl74c12.s1 Homo sapiens cDNA clone 43851 3'), M86526 (Rat proline-rich protein (PRP) gene, 5' end, and containing several Alu-like repetitive elements), M86514 (Rat proline-rich protein mRNA, 3' end), W68823  
30 (zd37f04.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 342847 5'), and Z54386 (H.sapiens CpG island DNA genomic MseI fragment, clone 10g3, forward read cpg10g3.ft1a). The predicted amino acid sequence disclosed herein for dd119\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the



BLASTX search protocol. The predicted dd119\_4 protein demonstrated at least some similarity to sequences identified as AB011135 (KIAA0563 protein [Homo sapiens]) and M86526 (proline-rich protein [Rattus norvegicus]). The rat proline-rich protein (PRP) is encoded by a single-copy gene and is expressed in the ventral prostate of the rat, with the precursor protein product being cleaved into multiple proline-rich polypeptides. Based upon sequence similarity, dd119\_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the dd119\_4 protein sequence centered around amino acid 928 of SEQ ID NO:108.

dd119\_4 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 166 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "df202\_3"

A polynucleotide of the present invention has been identified as clone "df202\_3". df202\_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. df202\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "df202\_3 protein").

The nucleotide sequence of df202\_3 as presently determined is reported in SEQ ID NO:109, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the df202\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:110. Amino acids 17 to 29 of SEQ ID NO:110 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the df202\_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone df202\_3 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for df202\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. df202\_3 demonstrated at least some similarity with sequences identified as AA138679 (mq76g03.r1 Stratagene mouse melanoma (#937312) Mus musculus cDNA clone 584692 5'), AA283121 (zt17b05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 713361 3'), AA286996 (zs58c10.r1 NCI\_CGAP\_GCB1 Soares NbHTGBC Homo sapiens cDNA clone IMAGE 701682 5'), N54968 (yv38g01.s1 Homo sapiens cDNA clone 245040 3'), T20071 (Human gene signature HUMGS01213), and W28275 (44g12 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA). The predicted amino acid sequence disclosed herein for df202\_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol.

10 The predicted df202\_3 protein demonstrated at least some similarity to the sequence identified as Z81137 (W02D9.h [Caenorhabditis elegans]). Based upon sequence similarity, df202\_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the df202\_3 protein sequence, centered around amino

15 acids 55, 80, and 108 of SEQ ID NO:110, respectively.

#### Clone "km225\_1"

A polynucleotide of the present invention has been identified as clone "km225\_1". km225\_1 was isolated from a human adult retina cDNA library using methods which are

20 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. km225\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "km225\_1 protein").

25 The nucleotide sequence of km225\_1 as presently determined is reported in SEQ ID NO:111, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the km225\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:112. Amino acids 9 to 21 of SEQ ID NO:112 are a predicted leader/signal sequence, with the

30 predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the km225\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone km225\_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for km225\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. km225\_1 demonstrated at least some similarity with sequences identified as AA101603 (zk94h09.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490529 3' similar to contains Alu repetitive element; mRNA sequence). Based upon sequence similarity, km225\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "mj301\_1"

A polynucleotide of the present invention has been identified as clone "mj301\_1". mj301\_1 was isolated from a human adult lymph node cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. mj301\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "mj301\_1 protein").

The nucleotide sequence of mj301\_1 as presently determined is reported in SEQ ID NO:113, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the mj301\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:114. Amino acids 65 to 77 of SEQ ID NO:114 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 78. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the mj301\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone mj301\_1 should be approximately 2760 bp; however, a band of 550 bp has been detected in restriction digests, possibly due to an internal EcoRI or NotI restriction site in the clone.

The nucleotide sequence disclosed herein for mj301\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. mj301\_1 demonstrated at least some similarity with sequences identified as AA053085 (zl73d01.s1 Stratagene colon (#937204) Homo sapiens cDNA

clone 510241 3'), AA347293 (EST53566 Fetal heart II Homo sapiens cDNA 5' end), AA813287 (ai76a07.s1 Soares testis NHT Homo sapiens cDNA clone 1376724 3', mRNA sequence), R45713 (Ha117-f Homo sapiens cDNA clone a117-f), T20114 (Human gene signature HUMGS01258), U46278 (Human clone xs252 mRNA sequence), Z36823 (H.sapiens (xs170) mRNA), and Z36832 (H.sapiens (xs170) mRNA). The human xs170 sequence is differentially expressed in pancreatic cancer cells. The predicted amino acid sequence disclosed herein for mj301\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted mj301\_1 protein demonstrated at least some similarity to the sequence identified as U07818 (putative phospho-beta-glucosidase [Bacillus stearothermophilus]). Based upon sequence similarity, mj301\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the mj301\_1 protein sequence centered around amino acid 60 of SEQ ID NO:114.

#### Clone "ml10\_7"

A polynucleotide of the present invention has been identified as clone "ml10\_7". ml10\_7 was isolated from a human adult brain (caudate nucleus) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ml10\_7 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ml10\_7 protein").

The nucleotide sequence of ml10\_7 as presently determined is reported in SEQ ID NO:115, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ml10\_7 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:116. Amino acids 30 to 42 of SEQ ID NO:116 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 43. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ml10\_7 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ml10\_7 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for ml10\_7 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ml10\_7 demonstrated at least some similarity with sequences identified as AA411457 (zv30f06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755171 3'), AA411585 (zv30f06.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755171 5', mRNA sequence), AA485512 (zx90b02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810987 5'), R97588 (yq59b05.r1 Homo sapiens cDNA clone 200049 5' similar to contains MSR1 repetitive element), and T23020 (Human gene signature HUMGS04748). The predicted amino acid sequence disclosed herein for ml10\_7 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ml10\_7 protein demonstrated at least some similarity to the sequence identified as R56978 (Human myotonic dystrophy gene protein). Based upon sequence similarity, ml10\_7 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four additional potential transmembrane domains within the ml10\_7 protein sequence, centered approximately around amino acids 20, 55 (between residues 50 and 60), 85 (between residues 80 and 89), and 175 (between residues 169 and 180) of SEQ ID NO:116, respectively. ml10\_7 appears to represent one member of a group of multiple alternatively spliced transcripts.

#### Clone "my340\_1"

A polynucleotide of the present invention has been identified as clone "my340\_1". my340\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. my340\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "my340\_1 protein").

The nucleotide sequence of my340\_1 as presently determined is reported in SEQ ID NO:117, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the my340\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:118.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone my340\_1 should be approximately 1800 bp.

5        The nucleotide sequence disclosed herein for my340\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. my340\_1 demonstrated at least some similarity with sequences identified as AA469015 (nc79g10.r1 NCI\_CGAP\_Pr2 Homo sapiens cDNA clone IMAGE:783618), H85290 (yv86f01.r1 Homo sapiens cDNA clone 249625 5'), L29074  
10 (Homo sapiens fragile X mental retardation protein (FMR-1) gene (6 alternative splices), complete cds), M86699 (Human kinase (TTK) mRNA, complete cds), W19755 (zb38f08.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 305895 5'), W63667 (zc57h10.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 326467 5', mRNA sequence), and Z84478 (Human DNA sequence). The predicted amino  
15 acid sequence disclosed herein for my340\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted my340\_1 protein demonstrated at least some similarity to the sequence identified as M86699 (kinase [Homo sapiens]). The human TTK kinase can phosphorylate serine, threonine, and tyrosine hydroxyamino acids. Based upon sequence similarity,  
20 my340\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the my340\_1 protein sequence centered around amino acid 50 of SEQ ID NO:28.

#### Deposit of Clones

25        Clones bn365\_53, bo342\_2, dn721\_8, dn834\_1, pd278\_5, pe80\_1, pm113\_1, pm749\_8, pt31\_4, and pv296\_5 were deposited on May 7, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98752, from which each clone comprising a particular polynucleotide is obtainable.

30        Clones er311\_20, fh149\_12, pc201\_6, pl87\_1, and pm514\_4 were deposited on June 2, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty

and were given the accession number ATCC 98781, from which each clone comprising a particular polynucleotide is obtainable.

Clones co155\_12, fn189\_13, lv2\_47, ml243\_1, pm96\_9, pu261\_1, pw214\_15, qb56\_19, qc646\_1, qf116\_2, and qf662\_3 were deposited on July 2, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98808, from which each clone comprising a particular polynucleotide is obtainable.

Clones am748\_5, cj507\_1, cn922\_5, cw691\_11, cw1000\_2, cw1640\_1, d24\_1, dd426\_1, and di393\_2 were deposited on July 16, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98817, from which each clone comprising a particular polynucleotide is obtainable.

Clones dj167\_2, dw665\_4, dx146\_12, dx219\_13, fm3\_1, h225\_1, kj320\_1, ml236\_5, and pu282\_10, were deposited on July 16, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98818, from which each clone comprising a particular polynucleotide is obtainable.

Clones at94\_2, bf169\_13, bl152\_12, bz578\_1, cb123\_1, ch245\_1, cj378\_3, cw1481\_1, dd119\_4, df202\_3, km225\_1, mj301\_1, ml10\_7, and my340\_1 were deposited on July 22, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98822, from which each clone comprising a particular polynucleotide is obtainable.

Clone dj167\_19 was deposited on February 5, 1999 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number ATCC 207090, from which the dj167\_19 clone comprising a particular polynucleotide is obtainable.

All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 1.806.

Each clone has been transfected into separate bacterial cells (*E. coli*) in the composite deposits above. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Figures 1A and 1B, respectively. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* **19**: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* **9**: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

	<u>Clone</u>	<u>Probe Sequence</u>
25	bn365_53	SEQ ID NO:119
	bo342_2	SEQ ID NO:120
	dn721_8	SEQ ID NO:121
	dn834_1	SEQ ID NO:122
	pd278_5	SEQ ID NO:123
30	pe80_1	SEQ ID NO:124
	pm113_1	SEQ ID NO:125
	pm749_8	SEQ ID NO:126
	pt31_4	SEQ ID NO:127
	pv296_5	SEQ ID NO:128



	er311_20	SEQ ID NO:129
	fh149_12	SEQ ID NO:130
	pc201_6	SEQ ID NO:131
	pl87_1	SEQ ID NO:132
5	pm514_4	SEQ ID NO:133
	co155_12	SEQ ID NO:134
	fn189_13	SEQ ID NO:135
	lv2_47	SEQ ID NO:136
	ml243_1	SEQ ID NO:137
10	pm96_9	SEQ ID NO:138
	pu261_1	SEQ ID NO:139
	pw214_15	SEQ ID NO:140
	qb56_19	SEQ ID NO:141
	qc646_1	SEQ ID NO:142
15	qf116_2	SEQ ID NO:143
	qf662_3	SEQ ID NO:144
	am748_5	SEQ ID NO:145
	cj507_1	SEQ ID NO:146
	cn922_5	SEQ ID NO:147
20	cw691_11	SEQ ID NO:148
	cw1000_2	SEQ ID NO:149
	cw1640_1	SEQ ID NO:150
	d24_1	SEQ ID NO:151
	dd426_1	SEQ ID NO:152
25	di393_2	SEQ ID NO:153
	dj167_2	SEQ ID NO:154
	dw665_4	SEQ ID NO:155
	dx146_12	SEQ ID NO:156
	dx219_13	SEQ ID NO:157
30	fm3_1	SEQ ID NO:158
	h225_1	SEQ ID NO:159
	kj320_1	SEQ ID NO:160
	ml236_5	SEQ ID NO:161
	pu282_10	SEQ ID NO:162

	at94_2	SEQ ID NO:163
	bf169_13	SEQ ID NO:164
	bl152_12	SEQ ID NO:165
	bz578_1	SEQ ID NO:166
5	cb123_1	SEQ ID NO:167
	ch245_1	SEQ ID NO:168
	cj378_3	SEQ ID NO:169
	cw1481_1	SEQ ID NO:170
	dd119_4	SEQ ID NO:171
10	df202_3	SEQ ID NO:172
	km225_1	SEQ ID NO:173
	mj301_1	SEQ ID NO:174
	ml10_7	SEQ ID NO:175
	my340_1	SEQ ID NO:176

15

In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramidite) (Glen Research, cat. no. 10-1953)).

20

The design of the oligonucleotide probe should preferably follow these parameters:

- (a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;
- 25 (b) It should be designed to have a  $T_m$  of approx. 80 ° C (assuming 2° for each A or T and 4 degrees for each G or C).

The oligonucleotide should preferably be labeled with  $\gamma$ -<sup>32</sup>P ATP (specific activity 6000 Ci/mmole) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4e+6 dpm/pmole.

30

5 The bacterial culture containing the pool of full-length clones should preferably be thawed and 100  $\mu$ l of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100  $\mu$ g/ml. The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100  $\mu$ g/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

10 Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100  $\mu$ g/ml of yeast RNA, and 10 mM EDTA (approximately 15 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to 1e+6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. 20 A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated 25 using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, 30 as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to

the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

5           The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or  
10 other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

          The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are  
15 derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed  
20 herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

25           The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately labeled polynucleotides of the present invention to chromosomes *in situ*. It may also be possible to determine the corresponding chromosomal location for a disclosed polynucleotide by identifying significantly similar nucleotide sequences in public  
30 databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences disclosed herein, public database sequences having at least some similarity to the polynucleotide of the present invention have been listed by database accession number. Searches using the GenBank accession numbers of these public database sequences can

then be performed at an Internet site provided by the National Center for Biotechnology Information having the address <http://www.ncbi.nlm.nih.gov/UniGene/>, in order to identify "UniGene clusters" of overlapping sequences. Many of the "UniGene clusters" so identified will already have been mapped to particular chromosomal sites.

- 5           Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* **15**(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* **62**(1): 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* **58**: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided.
- 10           Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated,
- 15           through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, *Bioessays* **14**(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* **90**(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* **91**(2): 719-722;
- 20           all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* **336**: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably
- 25           are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).
- 30

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms, part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information. For example, the TopPredII computer program can be used to predict the location of transmembrane domains in an amino acid sequence, domains which are described by the location of the center of the transmembrane domain, with at least ten transmembrane amino acids on each side of the reported central residue(s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

In particular, sequence identity may be determined using WU-BLAST (Washington University BLAST) version 2.0 software, which builds upon WU-BLAST version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local alignment statistics, Doolittle *ed.*, *Methods in Enzymology* **266**: 460-480; Altschul *et al.*, 1990, Basic local alignment search tool, *Journal of Molecular Biology* **215**: 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, *Nature Genetics* **3**: 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, *Proc. Natl. Acad. Sci. USA* **90**: 5873-5877; all of which are incorporated by reference herein). WU-BLAST version 2.0 executable programs for several UNIX platforms can be downloaded from <ftp://blast.wustl.edu/blast/executables>. The complete suite of search programs (BLASTP, BLASTN, BLASTX, TBLASTN, and TBLASTX) is

provided at that site, in addition to several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or redistributed in any form or manner without the express written consent of the author; but the posted executables may otherwise be freely used for commercial, nonprofit, or academic purposes. In all search programs in the suite

5 -- BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX -- the gapped alignment routines are integral to the database search itself, and thus yield much better sensitivity and selectivity while producing the more easily interpreted output. Gapping can optionally be turned off in all of these programs, if desired. The default penalty (Q) for a gap of length one is Q=9 for proteins and BLASTP, and Q=10 for BLASTN, but may be changed to any

10 integer value including zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. The default per-residue penalty for extending a gap (R) is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any integer value including zero, one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one

15 through one hundred, etc. Any combination of values for Q and R can be used in order to align sequences so as to maximize overlap and identity while minimizing sequence gaps. The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

Species homologues of the disclosed polynucleotides and proteins are also

20 provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with

25 the given polynucleotide, and protein species homologues have at least 30% sequence identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Species

30 homologues may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian

species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes*, *Gorilla gorilla*, *Pongo pygmaeus*, *Hylobates concolor*, *Macaca mulatta*, *Papio papio*, *Papio hamadryas*, *Cercopithecus aethiops*, *Cebus capucinus*, *Aotus trivirgatus*, *Sanguinus oedipus*, *Microcebus murinus*, *Mus musculus*, *Rattus norvegicus*,  
5 *Cricetulus griseus*, *Felis catus*, *Mustela vison*, *Canis familiaris*, *Oryctolagus cuniculus*, *Bos taurus*, *Ovis aries*, *Sus scrofa*, and *Equus caballus*, for which genetic maps have been created allowing the identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species (O'Brien and Seuáñez, 1988, *Ann. Rev. Genet.* **22**: 323-351; O'Brien *et al.*, 1993, *Nature*  
10 *Genetics* **3**:103-112; Johansson *et al.*, 1995, *Genomics* **25**: 682-690; Lyons *et al.*, 1997, *Nature Genetics* **15**: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* **13**(10): 393-399; Carver and Stubbs, 1997, *Genome Research* **7**:1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides  
15 which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize  
20 overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

25 The present invention also includes polynucleotides that hybridize under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as  
30 stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.



Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) <sup>‡</sup>	Hybridization Temperature and Buffer <sup>†</sup>	Wash Temperature and Buffer <sup>†</sup>
5	A	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	<50	T <sub>B</sub> <sup>*</sup> ; 1xSSC	T <sub>B</sub> <sup>*</sup> ; 1xSSC
	C	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	<50	T <sub>D</sub> <sup>*</sup> ; 1xSSC	T <sub>D</sub> <sup>*</sup> ; 1xSSC
	E	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
	F	<50	T <sub>F</sub> <sup>*</sup> ; 1xSSC	T <sub>F</sub> <sup>*</sup> ; 1xSSC
10	G	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	<50	T <sub>H</sub> <sup>*</sup> ; 4xSSC	T <sub>H</sub> <sup>*</sup> ; 4xSSC
	I	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	<50	T <sub>J</sub> <sup>*</sup> ; 4xSSC	T <sub>J</sub> <sup>*</sup> ; 4xSSC
	K	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	<50	T <sub>L</sub> <sup>*</sup> ; 2xSSC	T <sub>L</sub> <sup>*</sup> ; 2xSSC
15	M	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	<50	T <sub>N</sub> <sup>*</sup> ; 6xSSC	T <sub>N</sub> <sup>*</sup> ; 6xSSC
	O	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
	P	<50	T <sub>P</sub> <sup>*</sup> ; 6xSSC	T <sub>P</sub> <sup>*</sup> ; 6xSSC
	Q	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	<50	T <sub>R</sub> <sup>*</sup> ; 4xSSC	T <sub>R</sub> <sup>*</sup> ; 4xSSC

‡: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

†: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH<sub>2</sub>PO<sub>4</sub>, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

\*T<sub>B</sub> - T<sub>R</sub>: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T<sub>m</sub>) of the hybrid, where T<sub>m</sub> is determined according to the following equations. For hybrids less than 18 base pairs in length, T<sub>m</sub>(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T<sub>m</sub>(°C) = 81.5 + 16.6(log<sub>10</sub>[Na<sup>+</sup>]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na<sup>+</sup>] is the concentration of sodium ions in the hybridization buffer ([Na<sup>+</sup>] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial

strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from the Eastman Kodak Company (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art

given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

## **USES AND BIOLOGICAL ACTIVITY**

5           The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies  
10       or vectors suitable for introduction of DNA).

### **Research Uses and Utilities**

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15           The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare  
20       with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for  
25       examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those  
30       described in Gyuris *et al.*, 1993, *Cell* 75: 791-803 and in Rossi *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* 94: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

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The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

#### Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

#### Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may

induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

- 10 Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

- 20 Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon  $\gamma$ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

- 25 Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., *Proc. Natl. Acad. Sci. U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991;

Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

#### Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease.



Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term

tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

5       The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as  
10       described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

15       Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms.  
20       Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from  
25       the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/*lpr/lpr* mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and  
30       murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune

response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$

microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated  
5 immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated  
10 immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without  
15 limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al.,  
20 J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnoli et al.,  
25 Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro*  
30 antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek,

D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

5 Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; 10 Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, 15 proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; 20 Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

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#### Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell 30 lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid

cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al., *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and

Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

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#### Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns,  
10 incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as  
15 well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal  
20 disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue  
25 destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in  
30 circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and

in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation



of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium ).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

#### Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin  $\alpha$  family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- $\beta$  group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

#### Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. *J. Clin. Invest.* 95:1370-1376, 1995; Lind et al.

APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

#### Hemostatic and Thrombolytic Activity

5 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting  
10 formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

15 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

#### Receptor/Ligand Activity

20 A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands,  
25 receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant  
30 receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

#### 10      Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

25

#### Cadherin/Tumor Invasion Suppressor Activity

Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved

extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this  
5 recognition site can change the specificity of a cadherin so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells  
10 become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas  
15 to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed  
20 in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the  
25 inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block  
30 the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995; Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

#### Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

#### Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s);

effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic  
5 lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another  
10 material or entity which is cross-reactive with such protein.

### **ADMINISTRATION AND DOSING**

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a  
15 pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the  
20 carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other  
25 agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor,  
30 thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical

compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

5 The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to  
10 present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the  
15 invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers  
20 in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein  
25 by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing,  
30 prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.



10930644.050699  
In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in  
5 combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If  
10 administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical  
15 composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is  
20 administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention.  
25 When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid  
30 form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present

invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1mg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. As used herein, the term "antibody" includes without limitation a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single-chain antibody, a CDR-grafted antibody, a humanized antibody, or fragments thereof which bind to the indicated protein.

Such term also includes any other species derived from an antibody or antibody sequence which is capable of binding the indicated protein.

Antibodies to a particular protein can be produced by methods well known to those skilled in the art. For example, monoclonal antibodies can be produced by generation of antibody-producing hybridomas in accordance with known methods (see for example, 5 Goding, 1983, *Monoclonal antibodies: principles and practice*, Academic Press Inc., New York; and Yokoyama, 1992, "Production of Monoclonal Antibodies" in *Current Protocols in Immunology*, Unit 2.5, Greene Publishing Assoc. and John Wiley & Sons). Polyclonal sera and antibodies can be produced by inoculation of a mammalian subject with the 10 relevant protein or fragments thereof in accordance with known methods. Fragments of antibodies, receptors, or other reactive peptides can be produced from the corresponding antibodies by cleavage of and collection of the desired fragments in accordance with known methods (see for example, Goding, *supra*; and Andrew et al., 1992, "Fragmentation of Immunoglobulins" in *Current Protocols in Immunology*, Unit 2.8, Greene Publishing 15 Assoc. and John Wiley & Sons). Chimeric antibodies and single chain antibodies can also be produced in accordance with known recombinant methods (see for example, 5,169,939, 5,194,594, and 5,576,184). Humanized antibodies can also be made from corresponding murine antibodies in accordance with well known methods (see for example, U.S. Patent Nos. 5,530,101, 5,585,089, and 5,693,762). Additionally, human antibodies may be 20 produced in non-human animals such as mice that have been genetically altered to express human antibody molecules (see for example Fishwild *et al.*, 1996, *Nature Biotechnology* **14**: 845-851; Mendez *et al.*, 1997, *Nature Genetics* **15**: 146-156 (erratum *Nature Genetics* **16**: 410); and U.S. Patents 5,877,397 and 5,625,126). Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide 25 immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. **85**, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. **211**, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful 30 diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where

abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

5 For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systemically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably  
10 be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the  
15 methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical  
20 applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium  
25 sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other  
30 ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropylmethylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect

the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

5 Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

10 Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
  - (a) the nucleotide sequence of SEQ ID NO:21;
  - (b) the nucleotide sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008;
  - (c) the nucleotide sequence of the full-length protein coding sequence of clone er311\_20 deposited under accession number ATCC 98781;
  - (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;
  - (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
  - (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;
  - (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
  - (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:21.
2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.
3. A host cell transformed with the polynucleotide of claim 2.
4. The host cell of claim 3, wherein said cell is a mammalian cell.
5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:

- (a) growing a culture of a host cell transformed with the polynucleotide of claim 2 in a suitable culture medium; and
- (b) purifying said protein from the culture.

6. A protein produced according to the process of claim 5.

7. An isolated polynucleotide encoding the protein of claim 6.

8. The polynucleotide of claim 7, wherein the polynucleotide comprises the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781.

9. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:22;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;
- the protein being substantially free from other mammalian proteins.

10. The protein of claim 9, wherein said protein comprises the amino acid sequence of SEQ ID NO:22.

11. A composition comprising the protein of claim 9 and a pharmaceutically acceptable carrier.

12. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:65;
- (b) the nucleotide sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827;
- (c) the nucleotide sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827;



- (d) the nucleotide sequence of the full-length protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;
- (f) the nucleotide sequence of a mature protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:66;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:65.

13. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:66;
- (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
- (c) the amino acid sequence encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;

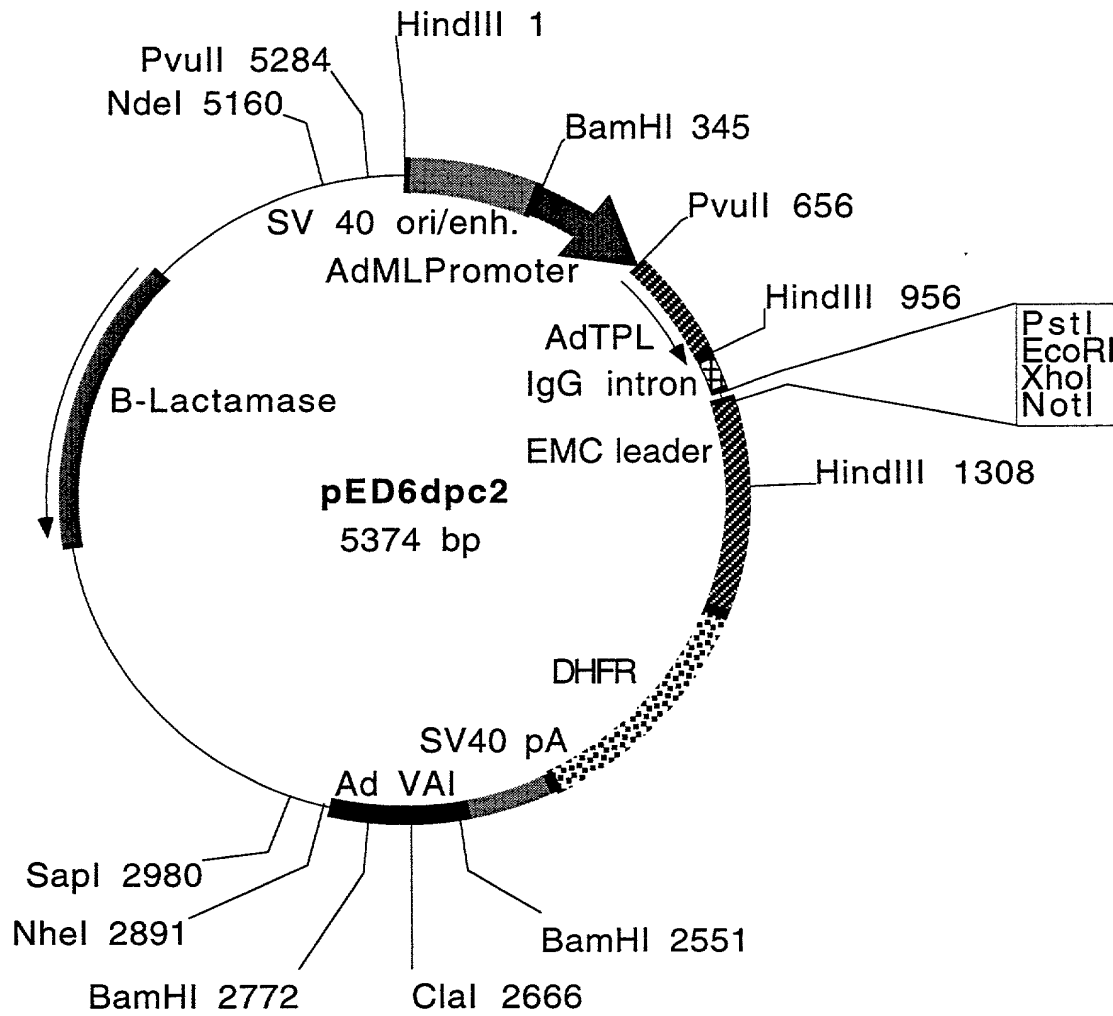
the protein being substantially free from other mammalian proteins.

### Abstract

Novel polynucleotides and the proteins encoded thereby are disclosed.

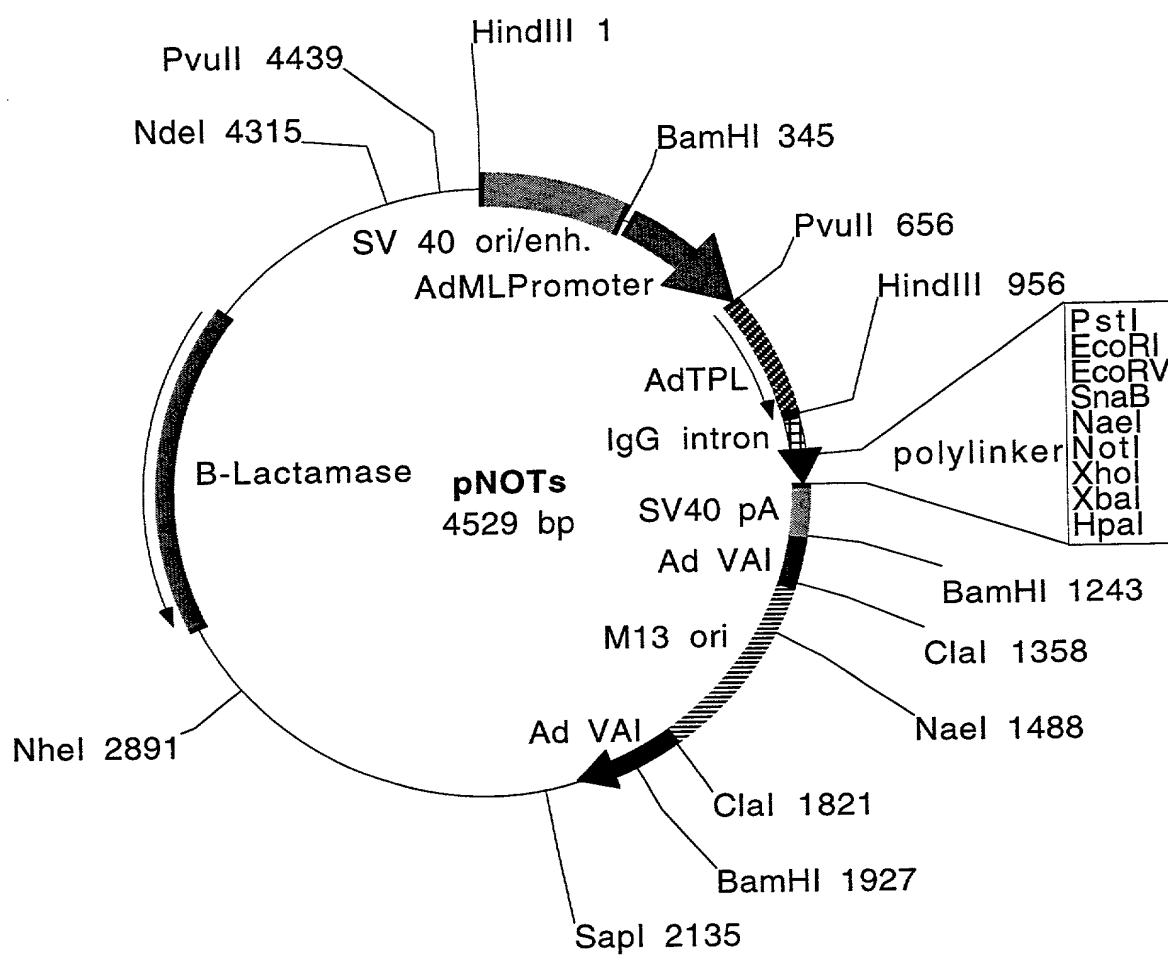
654050 T T 50850

Fig. 1A



665050-1190660

Fig. 1B



# SEQUENCE LISTING

<110> Jacobs, Kenneth  
McCoy, John M.  
LaVallie, Edward R.  
Collins-Racie, Lisa A.  
Evans, Cheryl  
Merberg, David  
Treacy, Maurice  
Agostino, Michael J.  
Steininger II, Robert J.  
Bowman, Michael R.  
DiBlasio-Smith, Elizabeth  
Widom, Angela  
Genetics Institute, Inc.

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"Express Mail" mailing label number: EL 37912356805

Date of Deposit May 6, 1999

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<210> 10  
 <211> 206  
 <212> PRT  
 <213> Homo sapiens

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 Ala Cys Thr Cys Leu Leu Asp Pro Ser Thr Trp Arg Pro Ala His Val  
 35 40 45

Ser Gly Pro Ala Leu Ala Ser Ser Pro Gln Ile Leu Ser Val Phe Ser  
 50 55 60  
 Leu Gly Phe Pro Gly Phe Val Asn Gly Ser Cys Val Ser Arg Tyr Lys  
 65 70 75 80  
 Pro Asp Ile Ile Ser Pro Pro Gly Leu Pro Pro Pro Asp Leu Pro Ser  
 85 90 95  
 Ser Val Ser Ile Phe Tyr Leu Gln Leu Leu Cys Ser His Gly His Cys  
 100 105 110  
 Cys Ile Thr Glu Ser Gly Pro Leu Leu Ser Phe Ser Asn Trp Pro Pro  
 115 120 125  
 Ser Leu Val Pro His Phe Leu Lys Ser Pro Val His Cys His Gln Ile  
 130 135 140  
 Lys Leu Ser Pro Ala Arg Ser Pro Leu Ser Glu Lys Pro Pro Leu Thr  
 145 150 155 160  
 Trp Lys His His Cys Leu Ala His Ile Leu Thr Tyr Ser Pro Ser Arg  
 165 170 175  
 Leu Asp Pro His Thr Ser Phe Gln Pro Pro Leu Pro Leu His Ser Leu  
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 195 200 205

<210> 11  
 <211> 2216  
 <212> DNA  
 <213> Homo sapiens

<400> 11  
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 tgtttggttg ttttttggtt ttttttttaa ggtctcact cttttgcccc ggctggagtg 480  
 cagtggcaca atcacggctc ccaggctaat gtttttattt ttaatttgta attttttttt 540  
 tatttttttt gttgagatgg agttgctcca tgttgccacag gctgttctca aactcctaag 600  
 ctcaagccat ctgcctgcst tggcctcccc aagtgstggg attgtagaca taagccacct 660  
 caccagcct atgaatatct ttctaacatk gtaagaatga ggtaatgttt ccatcagtct 720  
 aatacagata tatttcttcc ctccaaaaca gtttatattg attgtttatt ttattttgat 780  
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 ggaagaattg ttttagaaag acaatattta aaacaccgca ctgccaatat attgatcctt 900  
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 cctttgggag gtggtccttg gtgcgtgat cttggtatac agtctttatt gtaagtctga 1260  
 taaaaaatgc taataaattt aatgtttttc ttccttaatt tattggcata gttcttcagg 1320

Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	Male	10.1	0	20
Marital Status	Married	15.3	0	20
Education	High School	5.2	0	12
Occupation	Unemployed	8.7	0	20
Income	\$15,000	\$10,000	\$0	\$40,000
Health Status	Good	12.4	0	20
Smoking Status	Non-smoker	10.5	0	20
Alcohol Consumption	Occasional	8.9	0	20
Exercise Frequency	Low	6.3	0	20
Stress Level	High	14.2	0	20
Sleep Quality	Poor	9.8	0	20
Depression Score	10.5	5.2	0	20
Anxiety Score	12.1	4.8	0	20
Life Satisfaction	15.6	6.1	0	20
Resilience Score	11.3	5.5	0	20
Self-Efficacy	13.7	4.9	0	20
Optimism	14.5	5.3	0	20
Gratitude	16.2	5.7	0	20
Forgiveness	17.1	6.2	0	20
Empathy	18.3	6.5	0	20
Compassion	19.1	6.8	0	20
Kindness	20.0	7.0	0	20
Generosity	19.5	6.9	0	20
Patience	18.8	6.6	0	20
Humility	17.9	6.3	0	20
Modesty	16.7	6.0	0	20
Shyness	15.4	5.6	0	20
Introversion	14.2	5.3	0	20
Extroversion	13.1	5.0	0	20
Sensitiveness	12.0	4.7	0	20
Emotional Stability	11.5	4.5	0	20
Impulsivity	10.8	4.2	0	20
Risk-Taking	10.2	4.0	0	20
Adventurousness	9.5	3.8	0	20
Curiosity	8.9	3.6	0	20
Imagination	8.3	3.4	0	20
Creativity	7.7	3.2	0	20
Innovation	7.1	3.0	0	20
Originality	6.5	2.8	0	20
Uniqueness	5.9	2.6	0	20
Individuality	5.3	2.4	0	20
Personality	4.7	2.2	0	20
Character	4.1	2.0	0	20
Identity	3.5	1.8	0	20
Selfhood	2.9	1.6	0	20
Individualism	2.3	1.4	0	20
Autonomy	1.7	1.2	0	20
Independence	1.1	1.0	0	20
Freedom	0.5	0.8	0	20
Liberty	0.0	0.6	0	20

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<400> 12
Met Leu Phe Ser Lys His Ser Phe Phe Thr Leu Leu Cys Gly Leu Asp
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Pro Ser Arg Asn Leu Leu Ile Gly Lys Arg Leu Gln Thr Pro Ala Val
      20                      25                      30

Cys Val Leu Gln Val His Ala Ala Lys Val Ile Pro Ala His Pro Cys
      35                      40                      45

Pro Val Ser Val Ser Phe Arg Val Ile Pro Tyr Leu Ser Ile Gly Gly
  50                      55                      60

Leu Ile Leu Leu Asp Phe Leu Lys Thr Leu Arg Trp Ser Ile Arg Ser
  65                      70                      75                      80

Asp Phe Ser His Ser Ser Ala Gly Glu Leu Arg Ile Thr Ser Ser Phe
      85                      90                      95

Gly Arg Trp Ser Trp Val Arg Gly Ser Trp Tyr Thr Val Phe Ile Val
      100                      105                      110

Ser Leu Ile Gln Asn Ala Asn Lys Phe Asn Val Phe Leu Pro
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tcccagacca tggcctctgc tagctcacc ttgaaggagc ccccacatc ctcccctaca 180
tcccagagat gccaccactt gtgtctccac aatgtgtctc tgcccaccg ggttcgcgac 240
tgtccgacct ctgcacacca ctcattgtac cacggcgtgc atcatgttca tcccacatca 300
tttatttaag cctttcttgg cttgtagggc attttgatgt tagagcagtt gaaaacagaa 360
ctccagaact taacatctgt cctgatgtta aagtctttt catgaccacc ctgttatcta 420
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actttcctgt gggctcgctca gggcctcata gcatctcatt caattacaag aatagaggcc 660
agacacggtg gcgcatgcct gtagtcccag ctaactggga ggctgaggca ggaggatcac 720
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<210> 14
<211> 80
<212> PRT
<213> Homo sapiens

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<400> 14
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Ala Leu Ser Asp Pro Cys Thr Pro Leu Met Ser Pro Arg Arg Ala Ser
      20             25             30

Cys Ser Ser Pro Ser Ile Tyr Leu Ser Leu Ser Leu Leu Val Gly His
      35             40             45

Phe Val Cys Arg Ala Val Glu Asn Arg Thr Ser Glu Leu Asn Ile Cys
      50             55             60

Pro Asp Val Lys Val Leu Phe Met Thr Thr Leu Leu Ser Met Tyr Met
      65             70             75             80

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<210> 15
<211> 2364
<212> DNA
<213> Homo sapiens

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<400> 15
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ccccttacat cggcagcaag atcagcctca tctccaaggc ggagatccgc tacgagggca 180
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<210> 16  
 <211> 463  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
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 Asn Ser Thr Val Ala Leu Ala Lys Val Arg Ser Phe Gly Thr Glu Asp  
 35 40 45  
 Arg Pro Thr Asp Arg Pro Ile Pro Pro Arg Asp Glu Val Phe Glu Tyr  
 50 55 60  
 Ile Ile Phe Arg Gly Ser Asp Ile Lys Asp Leu Thr Val Cys Glu Pro  
 65 70 75 80  
 Pro Lys Pro Gln Cys Ser Leu Pro Gln Asp Pro Ala Ile Val Gln Ser  
 85 90 95  
 Ser Leu Gly Ser Ser Thr Ser Ser Phe Gln Ser Met Gly Ser Tyr Gly  
 100 105 110  
 Pro Phe Gly Arg Met Pro Thr Tyr Ser Gln Phe Ser Pro Ser Ser Leu  
 115 120 125  
 Val Gly Gln Gln Phe Gly Ala Val Gly Val Ala Gly Ser Ser Leu Thr  
 130 135 140



<210> 17  
 <211> 2760  
 <212> DNA  
 <213> Homo sapiens

<400> 17  
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<210> 18  
 <211> 660  
 <212> PRT  
 <213> Homo sapiens

<400> 18

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Ser	Pro	Arg	Val	Gln	Arg	Gln	Val	Thr	Ser	Leu	Leu	Arg	Arg	Val	Leu	35	40	45	
Pro	Glu	Val	Thr	Pro	Ser	Arg	Leu	Ala	Ser	Ile	Ile	Gly	Val	Lys	Ser	50	55	60	
Leu	Pro	Pro	Ala	Asp	Ile	Ser	Asp	Ile	Ile	His	Ser	Thr	Glu	Lys	Gly	65	70	75	80
Asp	Trp	Asn	Lys	Leu	Gly	Ile	Leu	Asp	Met	Phe	Leu	Gly	Cys	Ile	Ala	85	90	95	
Lys	Ala	Leu	Thr	Val	Gln	Leu	Lys	Ala	Lys	Gly	Thr	Thr	Ile	Thr	Gly	100	105	110	
Thr	Ala	Gly	Thr	Thr	Val	Gly	Lys	Gly	Val	Thr	Thr	Val	Thr	Leu	Pro	115	120	125	
Met	Ile	Phe	Asn	Ser	Ser	Tyr	Leu	Arg	Arg	Gly	Glu	Ser	His	Trp	Trp	130	135	140	
Met	Lys	Gly	Ser	Thr	Pro	Thr	Gln	Ile	Ser	Glu	Ile	Ile	Ile	Lys	Leu	145	150	155	160
Ile	Lys	Asp	Met	Ala	Ala	Gly	His	Leu	Ser	Glu	Ala	Trp	Ser	Arg	Val	165	170	175	
Thr	Lys	Asn	Ala	Ile	Ala	Glu	Thr	Ile	Ile	Ala	Leu	Thr	Lys	Met	Glu	180	185	190	
Glu	Glu	Phe	Arg	Ser	Pro	Val	Arg	Cys	Ile	Ala	Thr	Thr	Arg	Leu	Trp	195	200	205	
Leu	Ala	Leu	Ala	Ser	Leu	Cys	Val	Leu	Asp	Gln	Asp	His	Val	Asp	Arg	210	215	220	
Leu	Ser	Ser	Gly	Arg	Trp	Met	Gly	Lys	Asp	Gly	Gln	Gln	Lys	Gln	Met	225	230	235	240
Pro	Met	Cys	Asp	Asn	His	Asp	Asp	Gly	Glu	Thr	Ala	Ala	Ile	Ile	Leu	245	250	255	
Cys	Asn	Val	Cys	Gly	Asn	Leu	Cys	Thr	Asp	Cys	Asp	Arg	Phe	Leu	His	260	265	270	
Leu	His	Arg	Arg	Thr	Lys	Thr	His	Gln	Arg	Gln	Val	Phe	Lys	Glu	Glu	275	280	285	
Glu	Glu	Ala	Ile	Lys	Val	Asp	Leu	His	Glu	Gly	Cys	Gly	Arg	Thr	Lys	290	295	300	
Leu	Phe	Trp	Leu	Met	Ala	Leu	Ala	Asp	Ser	Lys	Thr	Met	Lys	Ala	Met	305	310	315	320

Val	Glu	Phe	Arg	Glu	His	Thr	Gly	Lys	Pro	Thr	Thr	Ser	Ser	Ser	Glu	325	330	335	
Ala	Cys	Arg	Phe	Cys	Gly	Ser	Arg	Ser	Gly	Thr	Glu	Leu	Ser	Ala	Val	340	345	350	
Gly	Ser	Val	Cys	Ser	Asp	Ala	Asp	Cys	Gln	Glu	Tyr	Ala	Lys	Ile	Ala	355	360	365	
Cys	Ser	Lys	Thr	His	Pro	Cys	Gly	His	Pro	Cys	Gly	Gly	Val	Lys	Asn	370	375	380	
Glu	Glu	His	Cys	Leu	Pro	Cys	Leu	His	Gly	Cys	Asp	Lys	Ser	Ala	Thr	385	390	395	400
Ser	Leu	Lys	Gln	Asp	Ala	Asp	Asp	Met	Cys	Met	Ile	Cys	Phe	Thr	Glu	405	410	415	
Ala	Leu	Ser	Ala	Ala	Pro	Ala	Ile	Gln	Leu	Asp	Cys	Ser	His	Ile	Phe	420	425	430	
His	Leu	Gln	Cys	Cys	Arg	Arg	Val	Leu	Glu	Asn	Arg	Trp	Leu	Gly	Pro	435	440	445	
Arg	Ile	Thr	Phe	Gly	Phe	Ile	Ser	Cys	Pro	Ile	Cys	Lys	Asn	Lys	Ile	450	455	460	
Asn	His	Ile	Val	Leu	Lys	Asp	Leu	Leu	Asp	Pro	Ile	Lys	Glu	Leu	Tyr	465	470	475	480
Glu	Asp	Val	Arg	Arg	Lys	Ala	Leu	Met	Arg	Leu	Glu	Tyr	Glu	Gly	Leu	485	490	495	
His	Lys	Ser	Glu	Ala	Ile	Thr	Thr	Pro	Gly	Val	Arg	Phe	Tyr	Asn	Asp	500	505	510	
Pro	Ala	Gly	Tyr	Ala	Met	Asn	Arg	Tyr	Ala	Tyr	Tyr	Val	Cys	Tyr	Lys	515	520	525	
Cys	Arg	Lys	Ala	Tyr	Phe	Gly	Gly	Glu	Ala	Arg	Cys	Asp	Ala	Glu	Ala	530	535	540	
Gly	Arg	Gly	Asp	Asp	Tyr	Asp	Pro	Arg	Glu	Leu	Ile	Cys	Gly	Ala	Cys	545	550	555	560
Ser	Asp	Val	Ser	Arg	Ala	Gln	Met	Cys	Pro	Lys	His	Gly	Thr	Asp	Phe	565	570	575	
Leu	Glu	Tyr	Lys	Cys	Arg	Tyr	Cys	Cys	Ser	Val	Ala	Val	Phe	Phe	Cys	580	585	590	
Phe	Gly	Thr	Thr	His	Phe	Cys	Asn	Ala	Cys	His	Asp	Asp	Phe	Gln	Arg	595	600	605	
Met	Thr	Ser	Ile	Pro	Lys	Glu	Glu	Leu	Pro	His	Cys	Pro	Ala	Gly	Pro	610	615	620	
Lys	Gly	Lys	Gln	Leu	Glu	Gly	Thr	Glu	Cys	Pro	Leu	His	Val	Val	His	625	630	635	640

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645 650 655

Ala His Thr Phe  
660

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<211> 1649  
<212> DNA  
<213> Homo sapiens

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gcggacacat ggagctcccc ttgtgggggg gccccctcca ttacccgacc taccgccctt 240  
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<212> PRT  
<213> Homo sapiens

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Tyr Ile Asn Ile Ser Ile Phe Phe Leu Gln Asn Gln Phe Ile Asn Gly  
35 40 45  
Arg Gly Val Trp Gly Gly His Met Glu Leu Pro Leu Trp Gly Gly Pro  
50 55 60

Leu His Tyr Pro Thr Tyr Arg Pro Phe Pro His Pro Pro Pro His Ser  
65 70 75 80

Pro Pro Pro Gly Cys Asp Cys Cys Lys Met Gly Val  
85 90

<210> 21  
<211> 2644  
<212> DNA  
<213> Homo sapiens

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gaagggcggc actatccttg gcacccgtag cttgaaaggg acgagttact gccttttcgg 420  
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gctgcagcac agggcgctccg gccctgacgg agaatgcgac agcaacgggc cgggcttcta 540  
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cacctactgt caggtccacg ttggcctagt tgttcgcttt ggaggcagca cccggctctt 660  
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aaaa 2644

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<211> 667  
 <212> PRT  
 <213> Homo sapiens

<220>  
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 35 40 45  
 Glu Gly Pro Thr Ala Leu Gln Asp Ser Asn Ser Gly Glu Pro Asp Ile  
 50 55 60  
 Pro Pro Pro Gln Pro Asp Cys Gly Asp Phe Arg Ser Leu Gln Glu Glu  
 65 70 75 80  
 Gln Ser Arg Pro Thr Thr Ala Val Ser Ser Pro Gly Gly Pro Ala Arg  
 85 90 95  
 Ala Pro Pro Tyr Gln Glu Pro Pro Trp Gly Gly Pro Ala Thr Ala Pro  
 100 105 110  
 Tyr Ser Leu Glu Thr Leu Lys Gly Gly Thr Ile Leu Gly Thr Arg Ser  
 115 120 125  
 Leu Lys Gly Thr Ser Tyr Cys Leu Phe Gly Arg Leu Ser Gly Cys Asp  
 130 135 140  
 Val Cys Leu Glu His Pro Ser Val Ser Arg Tyr His Ala Val Leu Gln  
 145 150 155 160  
 His Arg Ala Ser Gly Pro Asp Gly Glu Cys Asp Ser Asn Gly Pro Gly  
 165 170 175  
 Phe Tyr Leu Tyr Asp Leu Gly Ser Thr His Gly Thr Phe Leu Asn Lys  
 180 185 190  
 Thr Arg Ile Pro Pro Arg Thr Tyr Cys Arg Val His Val Gly His Val  
 195 200 205  
 Val Arg Phe Gly Gly Ser Thr Arg Leu Phe Ile Leu Gln Gly Pro Glu  
 210 215 220  
 Glu Asp Arg Glu Ala Glu Ser Glu Leu Thr Val Thr Gln Leu Lys Glu  
 225 230 235 240  
 Leu Arg Lys Gln Gln Gln Ile Leu Leu Xaa Lys Lys Met Leu Gly Glu  
 245 250 255  
 Asp Ser Asp Glu Glu Glu Met Asp Thr Ser Glu Arg Lys Ile Asn  
 260 265 270



Ala Gly Ser Gln Asp Asp Glu Met Gly Cys Thr Trp Gly Met Gly Glu  
 275 280 285  
 Asp Ala Val Glu Asp Asp Ala Glu Glu Asn Pro Ile Val Leu Glu Phe  
 290 295 300  
 Gln Gln Glu Arg Glu Ala Phe Tyr Ile Lys Asp Pro Lys Lys Ala Leu  
 305 310 315 320  
 Gln Gly Phe Phe Asp Arg Glu Gly Glu Glu Leu Glu Tyr Glu Phe Asp  
 325 330 335  
 Glu Gln Gly His Ser Thr Trp Leu Cys Arg Val Arg Leu Pro Val Asp  
 340 345 350  
 Asp Ser Thr Gly Lys Gln Leu Val Ala Glu Ala Ile His Ser Gly Lys  
 355 360 365  
 Lys Lys Glu Ala Met Ile Gln Cys Ser Leu Glu Ala Cys Arg Ile Leu  
 370 375 380  
 Asp Thr Leu Gly Leu Leu Arg Gln Glu Ala Val Ser Arg Lys Arg Lys  
 385 390 395 400  
 Ala Lys Asn Trp Glu Asp Glu Asp Phe Tyr Asp Ser Asp Asp Asp Thr  
 405 410 415  
 Phe Leu Asp Arg Thr Gly Leu Ile Glu Lys Lys Arg Leu Asn Arg Met  
 420 425 430  
 Lys Lys Ala Gly Lys Ile Asp Glu Lys Pro Glu Thr Phe Glu Ser Leu  
 435 440 445  
 Val Ala Lys Leu Asn Asp Ala Glu Arg Glu Leu Ser Glu Ile Ser Glu  
 450 455 460  
 Arg Leu Lys Ala Ser Ser Gln Val Leu Ser Glu Ser Pro Ser Gln Asp  
 465 470 475 480  
 Ser Leu Asp Ala Phe Met Ser Glu Met Lys Ser Gly Ser Thr Leu Asp  
 485 490 495  
 Gly Val Ser Arg Lys Lys Leu His Leu Arg Thr Phe Glu Leu Arg Lys  
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 Glu Gln Gln Arg Leu Lys Gly Leu Ile Lys Ile Val Lys Pro Ala Glu  
 515 520 525  
 Ile Pro Glu Leu Lys Lys Thr Glu Thr Gln Thr Thr Gly Ala Glu Asn  
 530 535 540  
 Lys Ala Lys Lys Leu Thr Leu Pro Leu Phe Gly Ala Met Lys Gly Gly  
 545 550 555 560  
 Ser Lys Phe Lys Leu Lys Thr Gly Thr Val Gly Lys Leu Pro Pro Lys  
 565 570 575  
 Arg Pro Glu Leu Pro Pro Thr Leu Met Arg Met Lys Asp Glu Pro Glu  
 580 585 590

Val Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Lys Glu Lys Glu  
595 600 605

Glu His Glu Lys Lys Lys Leu Glu Asp Gly Ser Leu Ser Arg Pro Gln  
610 615 620

Pro Glu Ile Glu Pro Glu Ala Ala Val Gln Glu Met Arg Pro Pro Thr  
625 630 635 640

Asp Leu Thr His Phe Lys Glu Thr Gln Thr His Gly Asn Ile Phe Leu  
645 650 655

Leu Leu Pro Val Leu Phe Ser Gly Gln Leu His  
660 665

<210> 23  
<211> 2402  
<212> DNA  
<213> Homo sapiens

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<210> 24  
 <211> 520  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
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 Ala Ser Gly Val Ser Val Ala Ser Ala Ala Leu Ala Ala Ser Ala Ala  
 35 40 45  
 Ser Arg Val Ala Thr Ser Thr Asp Pro Ser Cys Ser Gly Phe Ala Pro  
 50 55 60  
 Pro Asp Phe Asn His Cys Leu Lys Asp Trp Asp Tyr Asn Gly Leu Pro  
 65 70 75 80  
 Val Leu Thr Thr Asn Ala Ile Gly Gln Trp Asp Leu Val Cys Asp Leu  
 85 90 95  
 Gly Trp Gln Val Ile Leu Glu Gln Ile Leu Phe Ile Leu Gly Phe Ala  
 100 105 110  
 Ser Gly Tyr Leu Phe Leu Gly Tyr Pro Ala Asp Arg Phe Gly Arg Arg  
 115 120 125  
 Gly Ile Val Leu Leu Thr Leu Gly Leu Val Gly Pro Cys Gly Val Gly  
 130 135 140  
 Gly Ala Ala Ala Gly Ser Ser Thr Gly Val Met Ala Leu Arg Phe Leu  
 145 150 155 160  
 Leu Gly Phe Leu Leu Ala Gly Val Asp Leu Gly Val Tyr Leu Met Arg  
 165 170 175  
 Leu Glu Leu Cys Asp Pro Thr Gln Arg Leu Arg Val Ala Leu Ala Gly  
 180 185 190  
 Glu Leu Val Gly Val Gly Gly His Phe Leu Phe Leu Gly Leu Ala Leu  
 195 200 205  
 Val Ser Lys Asp Trp Arg Phe Leu Gln Arg Met Ile Thr Ala Pro Cys  
 210 215 220  
 Ile Leu Phe Leu Phe Tyr Gly Trp Pro Gly Leu Phe Leu Glu Ser Ala  
 225 230 235 240  
 Arg Trp Leu Ile Val Lys Arg Gln Ile Glu Glu Ala Gln Ser Val Leu  
 245 250 255  
 Arg Ile Leu Ala Glu Arg Asn Arg Pro His Gly Gln Met Leu Gly Glu  
 260 265 270

Glu Ala Gln Glu Ala Leu Gln Asp Leu Glu Asn Thr Cys Pro Leu Pro  
 275 280 285  
 Ala Thr Ser Ser Phe Ser Phe Ala Ser Leu Leu Asn Tyr Arg Asn Ile  
 290 295 300  
 Trp Lys Asn Leu Leu Ile Leu Gly Phe Thr Asn Phe Ile Ala His Ala  
 305 310 315 320  
 Ile Arg His Cys Tyr Gln Pro Val Gly Gly Gly Gly Ser Pro Ser Asp  
 325 330 335  
 Phe Tyr Leu Cys Ser Leu Leu Ala Ser Gly Thr Ala Ala Leu Ala Cys  
 340 345 350  
 Val Phe Leu Gly Val Thr Val Asp Arg Phe Gly Arg Arg Gly Ile Leu  
 355 360 365  
 Leu Leu Ser Met Thr Leu Thr Gly Ile Ala Ser Leu Val Leu Leu Gly  
 370 375 380  
 Leu Trp Asp Tyr Leu Asn Glu Ala Ala Ile Thr Thr Phe Ser Val Leu  
 385 390 395 400  
 Gly Leu Phe Ser Ser Gln Ala Ala Ala Ile Leu Ser Thr Leu Leu Ala  
 405 410 415  
 Ala Glu Val Ile Pro Thr Thr Val Arg Gly Arg Gly Leu Gly Leu Ile  
 420 425 430  
 Met Ala Leu Gly Ala Leu Gly Gly Leu Ser Gly Pro Ala Gln Arg Leu  
 435 440 445  
 His Met Gly His Gly Ala Phe Leu Gln His Val Val Leu Ala Ala Cys  
 450 455 460  
 Ala Leu Leu Cys Ile Leu Ser Ile Met Leu Leu Pro Glu Thr Lys Arg  
 465 470 475 480  
 Lys Leu Leu Pro Glu Val Leu Arg Asp Gly Glu Leu Cys Arg Arg Pro  
 485 490 495  
 Ser Leu Leu Arg Gln Pro Pro Pro Thr Arg Cys Asp His Val Pro Leu  
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 Leu Ala Thr Pro Asn Pro Ala Leu  
 515 520

<210> 25  
 <211> 2377  
 <212> DNA  
 <213> Homo sapiens

<400> 25  
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 cacagtcctt gctgcaatga ccagtcatga cttatgaag tttgttgccc catttaacga 180  
 agtaattgaa caaatgaaaa ttatcagaga ctctactccc aaccaatata tgggtgctgat 240

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caactcaata gaagatgacg tttgccagct agtgtatgtg gaaagagctg aagtgtctca 360
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 <212> PRT  
 <213> Homo sapiens

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                   20                  25                  30  
 Ser His Asp Leu Met Lys Phe Val Ala Pro Phe Asn Glu Val Ile Glu  
           35                  40                  45  
 Gln Met Lys Ile Ile Arg Asp Ser Thr Pro Asn Gln Tyr Met Val Leu  
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 Ile Lys Phe Arg Ala Gln Ala Asp Ala Asp Ser Phe Tyr Met Thr Cys  
   65                  70                  75                  80  
 Asn Gly Arg Gln Phe Asn Ser Ile Glu Asp Asp Val Cys Gln Leu Val  
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Tyr Val Glu Arg Ala Glu Val Leu Lys Ser Glu Asp Gly Ala Ser Leu  
100 105 110

Pro Val Met Asp Leu Thr Glu Leu Pro Lys Cys Thr Val Cys Leu Glu  
115 120 125

Arg Met Asp Glu Ser Val Asn Gly Ile Leu Thr Thr Leu Cys Asn His  
130 135 140

Ser Phe His Ser Gln Cys Leu Gln Arg Trp Asp Asp Thr Thr Cys Pro  
145 150 155 160

Val Cys Arg Tyr Cys Gln Thr Pro Glu Pro Val Glu Glu Asn Lys Cys  
165 170 175

Phe Glu Cys Gly Val Gln Glu Asn Leu Trp Ile Cys Leu Ile Cys Gly  
180 185 190

His Ile Gly Cys Gly Arg Tyr Val Ser Arg His Ala Tyr Lys His Phe  
195 200 205

Glu Glu Thr Gln His Thr Tyr Ala Met Gln Leu Thr Asn His Arg Val  
210 215 220

Trp Asp Tyr Ala Gly Asp Asn Tyr Val His Arg Leu Val Ala Ser Lys  
225 230 235 240

Thr Asp Gly Lys Ile Val Gln Tyr Glu Cys Glu Gly Asp Thr Cys Gln  
245 250 255

Glu Glu Lys Ile Asp Ala Leu Gln Leu Glu Tyr Ser Tyr Leu Leu Thr  
260 265 270

Ser Gln Leu Glu Ser Gln Arg Ile Tyr Trp Glu Asn Lys Ile Val Arg  
275 280 285

Ile Glu Lys Asp Thr Ala Glu Glu Ile Asn Asn Met Lys Thr Lys Phe  
290 295 300

Lys Glu Thr Ile Glu Lys Cys Asp Asn Leu Glu His Lys Leu Asn Asp  
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Leu Leu Lys Glu Lys Gln Ser Val Glu Arg Lys Cys Thr Gln Leu Asn  
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<213> Homo sapiens

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 460

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 <211> 85  
 <212> PRT  
 <213> Homo sapiens

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 Ala Ala Asn Glu Lys Pro Phe Met Gln Thr Phe Leu Thr Ile Leu Lys  
 35 40 45  
 Ile Phe Leu Met Met Met Thr Ser Ser Glu Met Pro Ser Gly Cys Arg  
 50 55 60  
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 65 70 75 80  
 Ser Phe Arg Trp Phe  
 85

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 <211> 3204  
 <212> DNA  
 <213> Homo sapiens

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Gly Ser Asp Glu Lys Lys Ser Val Lys Thr Val Asn Gln Leu Ala His  
130 135 140

Ala Leu His Met Asp Lys Asp Leu Lys Ala Gly Cys Leu Val Arg Val  
145 150 155 160

Phe Trp Pro Lys Ala Lys Cys Ala Leu Leu Arg Asp Asp Leu Val Leu  
165 170 175

Val Asp Ser Pro Gly Thr Asp Val Thr Thr Glu Leu Asp Ser Trp Ile  
180 185 190

Asp Lys Phe Cys Leu Asp Ala Asp Val Phe Val Leu Val Ala Asn Ser  
195 200 205

Glu Ser Thr Leu Met Asn Thr Glu Lys His Phe Phe His Lys Val Asn  
210 215 220

Glu Arg Leu Ser Lys Pro Asn Ile Phe Ile Leu Asn Asn Arg Trp Asp  
225 230 235 240

Ala Ser Ala Ser Glu Pro Glu Tyr Met Glu Asp Val Arg Arg Gln His  
245 250 255

Met Glu Arg Cys Leu His Phe Leu Val Glu Glu Leu Lys Val Val Asn  
260 265 270

Ala Leu Glu Ala Gln Asn Arg Ile Phe Phe Val Ser Ala Lys Glu Val  
275 280 285

Leu Ser Ala Arg Lys Gln Lys Ala Gln Gly Met Pro Glu Ser Gly Val  
290 295 300

Ala Leu Ala Glu Gly Phe His Ala Arg Leu Gln Glu Phe Gln Asn Phe  
305 310 315 320

Glu Gln Ile Phe Glu Glu Cys Ile Ser Gln Ser Ala Val Lys Thr Lys  
325 330 335

Phe Glu Gln His Thr Ile Arg Ala Lys Gln Ile Leu Ala Thr Val Lys  
340 345 350

Asn Ile Met Asp Ser Val Asn Leu Ala Ala Glu Asp Lys Arg His Tyr  
355 360 365

Ser Val Glu Glu Arg Glu Asp Gln Ile Asp Arg Leu Asp Phe Ile Arg  
370 375 380

Asn Gln Met Asn Leu Leu Thr Leu Asp Val Lys Lys Lys Ile Lys Glu  
385 390 395 400

Val Thr Glu Glu Val Ala Asn Lys Val Ser Cys Ala Met Thr Asp Glu  
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Ile Cys Arg Leu Ser Val Leu Val Asp Glu Phe Cys Ser Glu Phe His  
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Pro Asn Pro Asp Val Leu Lys Ile Tyr Lys Ser Glu Leu Asn Lys His  
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<211> 2483  
 <212> DNA  
 <213> Homo sapiens

<400> 31

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 <212> PRT  
 <213> Homo sapiens

<400> 32

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Arg Ser Asp Thr Asp Glu Glu Glu Asp Asn Lys Tyr Lys Pro Ser Ser  
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Ser Gly Leu Lys Pro Arg Ser Asn Val Ile Ser Tyr Val Thr Val Asn  
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Asp Ser Pro Asp Ser Asp Ser Ser Leu Ser Ser Pro Tyr Ser Thr Asp  
385 390 395 400

Thr Leu Ser Ala Leu Arg Gly Asn Ser Gly Ser Val Leu Glu Gly Pro  
405 410 415

Gly Arg Val Val Ala Asp Gly Thr Gly Thr Arg Thr Ile Ile Val Pro  
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Pro Leu Lys Thr Gln Leu Gly Asp Cys Thr Val Ala Thr Gln Ala Ser  
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Gly Leu Leu Ser Asn Lys Thr Lys Pro Val Ala Ser Val Ser Gly Gln  
450 455 460

Ser Ser Gly Cys Cys Ile Thr Pro Thr Gly Tyr Arg Ala Gln Arg Gly  
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Gly Thr Ser Ala Ala Gln Pro Leu Asn Leu Ser Gln Asn Gln Gln Ser  
485 490 495

Ser Ala Ala Pro Thr Ser Gln Glu Arg Ser Ser Asn Pro Ala Pro Arg  
500 505 510

Arg Gln Gln Ala Phe Val Ala Pro Leu Ser Gln Ala Pro Tyr Thr Phe  
515 520 525

Gln His Gly Ser Pro Leu His Ser Thr Gly His Pro His Leu Ala Pro  
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Ala Pro Ala His Leu Pro Ser Gln Ala His Leu Tyr Thr Tyr Ala Ala  
545 550 555 560

Pro Thr Ser Ala Ala Ala Leu Gly Ser Thr Ser Ser Ile Ala His Leu  
565 570 575

Phe Ser Pro Gln Gly Ser Ser Arg His Ala Ala Ala Tyr Thr Thr His  
580 585 590

Pro Ser Thr Leu Val His Gln Val Pro Val Ser Val Gly Pro Ser Leu  
595 600 605

Leu Thr Ser Ala Ser Val Ala Pro Ala Gln Tyr Gln His Gln Phe Ala  
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Thr Gln Ser Tyr Ile Gly Ser Ser Arg Gly Ser Thr Ile Tyr Thr Gly  
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<210> 33

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<222> (2173)

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Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser  
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Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr  
 50 55 60

Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile  
 65 70 75 80

Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe  
 85 90 95

Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu Lys Glu Lys Arg  
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Gly Leu Ser Gly Lys Tyr Gln Thr Ser Ser Lys Leu Phe Gln Asn Cys  
 115 120 125

Ser Glu Leu Phe Lys Thr Gln Thr Phe Ser Gly Asp Phe Met His Arg  
 130 135 140

Leu Pro Leu Leu Gly Glu Lys Gln Glu Ala Lys Glu Asn Gly Thr Asn  
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Leu Thr Phe Ile Gly Asp Lys Thr Ala Met His Glu Pro Leu Gln Thr  
 165 170 175

Trp Gln Asp Ala Pro Tyr Ile Phe Ile Val His Ile Gly Ile Ser Ser  
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Ser Lys Glu Ser Ser Lys Glu Asn Ser Leu Ser Asn Leu Phe Thr Met  
 195 200 205

Thr Val Glu Val Lys Gly Pro Tyr Glu Tyr Leu Thr Leu Glu Asp Tyr  
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Pro Leu Met Ile Phe Phe Met Val Met Cys Ile Val Tyr Val Leu Phe  
 225 230 235 240

Gly Val Leu Trp Leu Ala Trp Ser Ala Cys Tyr Trp Arg Asp Leu Leu  
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Arg Ile Gln Phe Trp Ile Gly Ala Val Ile Phe Leu Gly Met Leu Glu  
 260 265 270

Lys Ala Val Phe Tyr Ala Glu Phe Gln Asn Ile Arg His Lys Gly Glu  
 275 280 285

Ser Val Gln Gly Ala Leu Ile Leu Ala Glu Leu Leu Ser Ala Val Lys





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<211> 164  
<212> PRT  
<213> Homo sapiens

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Leu Gly Arg Pro Thr Pro Cys Ala Val Pro Gly Thr Gly Phe Ser Leu  
50 55 60  
Leu Ser Thr Cys Ser Ser Pro Arg Gly Pro Val Pro Glu Thr Gly Arg  
65 70 75 80  
Gly Trp Arg Val Pro Thr Pro Cys Ser Leu Pro Asp Leu Leu Arg Asp  
85 90 95  
Asp Asp Ala Val Cys Val Pro His Val Gly Pro Pro Pro Ala Cys His  
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115 120 125  
Trp Cys Ala Glu Leu His Trp Glu Asp Phe Gln Arg Gly Arg Ala Ala  
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<210> 37  
<211> 1493  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> (1415)

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<210> 38
<211> 132
<212> PRT
<213> Homo sapiens

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      20             25             30

Leu Ile Ala Tyr Cys Ser Gln Leu Ala Ala Gly Thr Cys Glu Ile Val
      35             40             45

Thr Leu Asp Arg Asp Ser Ser Gln Pro Arg Arg Thr Ile Ala Arg Gln
      50             55             60

Thr Ala Arg Cys Ala Cys Arg Lys Gly Gln Ile Ala Gly Thr Thr Arg
      65             70             75             80

Ala Arg Pro Ala Cys Val Asp Ala Arg Ile Ile Lys Thr Lys Gln Trp
      85             90             95

Cys Asp Met Leu Pro Cys Leu Glu Gly Glu Gly Cys Asp Leu Leu Ile
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Asn Arg Ser Gly Trp Thr Cys Thr Gln Pro Gly Gly Arg Ile Lys Thr
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Thr Thr Val Ser
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<210> 39
<211> 3693
<212> DNA
<213> Homo sapiens

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<220>  
 <221> unsure  
 <222> (108)

<400> 39

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 <211> 230  
 <212> PRT  
 <213> Homo sapiens

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                     20                    25                    30  
 Leu Pro Glu Gln Val Ala Glu Asp Ala Ile Asp Trp Gly Asp Phe Gly  
                     35                    40                    45  
 Val Glu Ala Val Ser Glu Gly Thr Asp Ser Gly Ile Ser Ala Glu Ala  
                     50                    55                    60  
 Ala Gly Ile Asp Trp Gly Ile Phe Pro Glu Ser Asp Ser Lys Asp Pro  
                     65                    70                    75                    80  
 Gly Gly Asp Gly Ile Asp Trp Gly Asp Asp Ala Val Ala Leu Gln Ile  
                     85                    90                    95  
 Thr Val Leu Glu Ala Gly Thr Gln Ala Pro Glu Gly Val Ala Arg Gly  
                     100                    105                    110  
 Pro Asp Ala Leu Thr Leu Leu Glu Tyr Thr Glu Thr Arg Asn Gln Phe  
                     115                    120                    125  
 Leu Asp Glu Leu Met Glu Leu Glu Ile Phe Leu Ala Gln Arg Ala Val  
                     130                    135                    140  
 Glu Leu Ser Glu Glu Ala Asp Val Leu Ser Val Ser Gln Phe Gln Leu  
                     145                    150                    155                    160  
 Ala Pro Ala Ile Leu Gln Gly Gln Thr Lys Glu Lys Met Val Thr Met  
                     165                    170                    175  
 Val Ser Val Leu Glu Asp Leu Ile Gly Lys Leu Thr Ser Leu Gln Leu  
                     180                    185                    190  
 Gln His Leu Phe Met Ile Leu Ala Ser Pro Arg Ser Gly Phe Pro Leu  
                     195                    200                    205  
 Met Gln Gly Ser Ala Ile Leu Ser Ser Ser Ala Ser Leu Tyr Ser Ser  
                     210                    215                    220  
 Ser Cys Ser Met Thr Pro  
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<210> 41  
 <211> 1701  
 <212> DNA  
 <213> Homo sapiens

<400> 41  
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<210> 42  
 <211> 240  
 <212> PRT  
 <213> Homo sapiens

<400> 42  
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 35 40 45  
 Gly Thr Glu Cys Val Leu Ser Ser Thr Gly Arg Thr Ala Ala Cys Phe  
 50 55 60  
 Leu Pro Thr Ser Leu Leu Pro Thr Ser Pro Ala Ala Trp Leu Gly Pro  
 65 70 75 80  
 Glu Ala Leu Cys Leu Pro Gly Arg Pro Gly Thr Thr Gly Leu Arg Asp  
 85 90 95

Thr Gly Gly Pro Leu Leu Leu Pro Pro Pro Thr Leu Leu Gln Asp Thr  
 100 105 110  
 Thr Arg Trp Cys Trp Met Leu Val Leu Trp Pro Ala Lys Val His Gly  
 115 120 125  
 Asp Ser Pro His Gly Ile Leu Arg Asp Gln Ala Ala Gly Ile Gly Lys  
 130 135 140  
 Glu Phe His Pro Asp Arg Cys Pro Ser Gln Val Pro Arg Arg Pro His  
 145 150 155 160  
 His Thr Pro Phe Gln Gly Gln Gly Ser Ser Lys Pro Arg Ala Arg Ile  
 165 170 175  
 Leu Cys Cys Cys Leu Val Glu Ser Leu Pro Pro Cys Val Gly Ser Val  
 180 185 190  
 Gly Gln Ala Glu Cys Ile Gly Asp Arg Ala Val Ser Met Gly Leu Gly  
 195 200 205  
 Val Cys Glu Leu Arg Pro Arg Cys Ala Val Trp Arg Arg Val Leu Ser  
 210 215 220  
 Gly Lys Arg Cys Gly Phe Lys Val Cys Val Cys Arg Gly Trp Val Cys  
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<210> 43  
 <211> 1784  
 <212> DNA  
 <213> Homo sapiens

<400> 43  
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<210> 44  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens

<400> 44  
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                   20                  25                  30  
 Pro Phe Ile Phe Phe Asn Asn Cys Ile Ser Ala Gln Val Ile His Tyr  
           35                  40                  45  
 Ser Leu Lys Pro Cys Leu Cys Asn Leu Thr Ser Asp Met Leu Ala Ile  
           50                  55                  60  
 Lys Ala Cys Thr Cys Asn Asn Glu Lys Glu Lys Ala Phe Tyr Ile Thr  
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<210> 45  
 <211> 1034  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (598)

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<210> 46

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<210> 47
<211> 1626
<212> DNA
<213> Homo sapiens
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44



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<210> 48  
<211> 368  
<212> PRT  
<213> Homo sapiens

<400> 48  
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Tyr Ile Phe Leu Cys Leu Met Cys Trp Val Arg Ser Asp Asn Lys Arg  
35 40 45  
Pro Cys Leu Glu Phe Ser Gln Leu Ser Val Lys Asp Ser Phe Arg Asp  
50 55 60  
Leu Phe Ile Pro Arg Ile Glu Thr Ile Leu Met Met Tyr Thr Arg Asn  
65 70 75 80  
Asn Leu Asn Cys Ala Glu Pro Leu Phe Glu Gln Asn Asn Ser Leu Asn  
85 90 95  
Val Asn Phe Asn Thr Gln Lys Lys Thr Val Trp Leu Ile His Gly Tyr  
100 105 110  
Arg Pro Val Gly Ser Ile Pro Leu Trp Leu Gln Asn Phe Val Arg Ile  
115 120 125  
Leu Leu Asn Glu Glu Asp Met Asn Val Ile Val Val Asp Trp Ser Arg  
130 135 140  
Gly Ala Thr Thr Phe Ile Tyr Asn Arg Ala Val Lys Asn Thr Arg Lys  
145 150 155 160  
Val Ala Val Ser Leu Ser Val His Ile Lys Asn Leu Leu Lys His Gly  
165 170 175  
Ala Ser Leu Asp Asn Phe His Phe Ile Gly Val Ser Leu Gly Ala His  
180 185 190  
Ile Ser Gly Phe Val Gly Lys Ile Phe His Gly Gln Leu Gly Arg Ile  
195 200 205  
Thr Gly Leu Asp Pro Ala Gly Pro Arg Phe Ser Arg Lys Pro Pro Tyr  
210 215 220  
Ser Arg Leu Asp Tyr Thr Asp Ala Lys Phe Val Asp Val Ile His Ser  
225 230 235 240  
Asp Ser Asn Gly Ile Gln Phe Ile Lys Cys Asn His Gln Arg Ala Val  
245 250 255  
His Leu Phe Met Ala Ser Leu Glu Thr Asn Cys Asn Phe Ile Ser Phe

260 265 270

Pro Cys Arg Ser Tyr Lys Asp Tyr Lys Thr Ser Leu Cys Val Asp Cys  
275 280 285

Asp Cys Phe Lys Glu Lys Ser Cys Pro Arg Leu Gly Tyr Gln Ala Lys  
290 295 300

Leu Phe Lys Gly Val Leu Lys Glu Arg Met Glu Gly Arg Pro Leu Arg  
305 310 315 320

Thr Thr Val Phe Leu Asp Thr Ser Ala Tyr Tyr Phe Val Leu Ser Ile  
325 330 335

Ile Val Pro Asp Lys Thr Met Met Asp Gly Ser Phe Ser Phe Lys Leu  
340 345 350

Leu Asn Gln Leu Gly Met Ile Glu Glu Pro Arg Leu Tyr Glu Glu Arg  
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<210> 49  
<211> 1221  
<212> DNA  
<213> Homo sapiens

<400> 49  
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agtgccatga agaactacga gattagcctg gatattaact tgtcttctag agaatagatt 180  
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<210> 50  
<211> 305  
<212> PRT  
<213> Homo sapiens

<400> 50  
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Asn Ile His Arg Gly Phe Tyr Cys Leu Thr Ala Ile Leu Pro Gln Ile  
20 25 30

Cys Ile Cys Ser Gln Phe Ser Val Pro Ser Ser Tyr His Phe Thr Glu  
 35 40 45  
 Asp Pro Gly Ala Phe Pro Val Ala Thr Asn Gly Glu Arg Phe Pro Trp  
 50 55 60  
 Gln Glu Leu Arg Leu Pro Ser Val Val Ile Pro Leu His Tyr Asp Leu  
 65 70 75 80  
 Phe Val His Pro Asn Leu Thr Ser Leu Asp Phe Val Ala Ser Glu Lys  
 85 90 95  
 Ile Glu Val Leu Val Ser Asn Ala Thr Gln Phe Ile Ile Leu His Ser  
 100 105 110  
 Lys Asp Leu Glu Ile Thr Asn Ala Thr Leu Gln Ser Glu Glu Asp Ser  
 115 120 125  
 Arg Tyr Met Lys Pro Gly Lys Glu Leu Lys Val Leu Ser Tyr Pro Ala  
 130 135 140  
 His Glu Gln Ile Ala Leu Leu Val Pro Glu Lys Leu Thr Pro His Leu  
 145 150 155 160  
 Lys Tyr Tyr Val Ala Met Asp Phe Gln Ala Lys Leu Gly Asp Gly Phe  
 165 170 175  
 Glu Gly Phe Tyr Lys Ser Thr Tyr Arg Thr Leu Gly Gly Glu Thr Arg  
 180 185 190  
 Ile Leu Ala Val Thr Asp Phe Glu Pro Thr Gln Ala Arg Met Ala Phe  
 195 200 205  
 Pro Cys Phe Asp Glu Pro Leu Phe Lys Ala Asn Phe Ser Ile Lys Ile  
 210 215 220  
 Arg Arg Glu Ser Arg His Ile Ala Leu Ser Asn Met Pro Lys Val Ser  
 225 230 235 240  
 Ile Tyr Ala Ser Pro Asp Lys Arg Asn Gln Thr His Tyr Ala Leu Gln  
 245 250 255  
 Ala Ser Leu Lys Leu Leu Asp Phe Tyr Glu Lys Tyr Phe Asp Ile Tyr  
 260 265 270  
 Tyr Pro Leu Ser Lys Leu Gly Met Phe Lys Phe His Ile Ile Val Phe  
 275 280 285  
 Ile Phe Ala His Lys Thr Cys Leu Asp Leu Phe Pro Leu Ser Leu Cys  
 290 295 300  
 Met  
 305

<210> 51  
 <211> 951  
 <212> DNA  
 <213> Homo sapiens

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<400> 51
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cggtcaccta cccccagcac cactccagc ccctgcgcct cggaggcaga cagtggggag 240
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gtagtgggtt caactaatgg tagacaagac actgaagaaa gcatcgtcct aggaatggat 540
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ctaattcatt tggatggtga tgggtgggttc agtgtatcga cggataacag agttcacata 660
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gatgtactat tgggtggaaga atgaactgga gcagcctttc tggagagtga tttgccaata 780
tgccttatca ttttgcatga tctttgtcct agtaactcta tttctatgga tttactctaa 840
gtttgtaaac atggatgtgt gcaaagattt tagctctaag aatgtttgtc agtgttctaa 900
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<210> 52
<211> 194
<212> PRT
<213> Homo sapiens

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<400> 52
Met Ala Leu Val Thr Val Gln Arg Ser Pro Thr Pro Ser Thr Thr Ser
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Ser Pro Cys Ala Ser Glu Ala Asp Ser Gly Glu Glu Glu Cys Arg Ser
          20                      25                      30

Gln Pro Arg Ser Ile Ser Glu Ser Phe Leu Thr Val Lys Gly Ala Ala
          35                      40                      45

Leu Phe Leu Pro Arg Gly Asn Gly Ser Ser Thr Pro Arg Ile Ser His
          50                      55                      60

Arg Arg Asn Lys His Ala Gly Asp Leu Gln Gln His Leu Gln Ala Met
          65                      70                      75                      80

Phe Ile Leu Leu Arg Pro Glu Asp Asn Ile Arg Leu Ala Val Arg Leu
          85                      90                      95

Glu Ser Thr Tyr Gln Asn Arg Thr Arg Tyr Met Val Val Val Ser Thr
          100                      105                      110

Asn Gly Arg Gln Asp Thr Glu Glu Ser Ile Val Leu Gly Met Asp Phe
          115                      120                      125

Ser Ser Asn Asp Ser Thr Cys Thr Met Gly Leu Val Leu Pro Leu Trp
          130                      135                      140

Ser Asp Thr Leu Ile His Leu Asp Gly Asp Gly Gly Phe Ser Val Ser
          145                      150                      155                      160

Thr Asp Asn Arg Val His Ile Phe Lys Pro Val Ser Val Gln Ala Met
          165                      170                      175

Trp Val Asp Arg Asp Ser Arg Asn Lys His Cys Asp Val Leu Leu Val
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Glu Glu

<210> 53  
<211> 1514  
<212> DNA  
<213> Homo sapiens

<400> 53  
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gattttgggg ttttttcaca ttgcgctatt cagtataaac ctgctctcaa cattcatgtg 180  
caagtctttg agtggacata tatttgcggt tctcttgagt gaatgcacct tgttgggtca 240  
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ttgcaaagt ttgttcaaat tcttcacctg tttttaatga agacgtacga cttatttttg 420  
tgttctgaac ataagttctt tgtcacataa aatgtgctat gaatgttgag ttttaaatac 480  
tccaaatgaa tggctagaga attactatct gtagaaatat ttatatgtca aagggatgct 540  
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aaaaaaaaaa aaaa 1514

<210> 54  
<211> 91  
<212> PRT  
<213> Homo sapiens

<400> 54  
Met Ala Ser Gln Val Pro Ser Ser Pro Phe Gln Ser Phe Phe Val Phe  
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Val Phe Val Phe Leu Arg Pro Ser His Ser Val Ala Gln Ala Gly Val  
20 25 30  
Pro Leu His Phe Tyr Phe Phe Ile Gln Gln Val Leu Ile Lys Cys Ala  
35 40 45  
Leu Tyr Gln Val Leu Ser Ser Ser Leu Gly Tyr Asn Gly Asp Gln Gly  
50 55 60  
Asp Cys Arg Phe Trp Gln Gly Lys Leu Thr Ser Asn Thr Ala Thr Arg  
65 70 75 80  
His Ser Glu Thr Leu Ser Leu Leu Glu Glu Leu

<210> 55  
 <211> 1417  
 <212> DNA  
 <213> Homo sapiens

<400> 55  
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 agcagtcaac caacatattt ctttcccaga gtcccatgaa taatcttcag actaacacag 180  
 tagcccaaga agcatttttt gcagcaccga actcaatttc tccacttcag tcaacatcaa 240  
 acagtgaaca acaagctgct ttccaacagc aagctccaat atcacacatc cagactccta 300  
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 aacagcagca gcaacagcag cagcaacaac aacagagcat tttattcagt aatcagaata 540  
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 aaaatccaat ggctaatacag gagcaacaga accagtcaat ttttcaccaa caaagtaaca 660  
 tggccccaat gaatcaagag caacagccca tgcaatttca gagtcagtcc acagtttctc 720  
 cacttcagaa cccaggtcct acccagtcgg aatcatcaca gaccccttg ttccatagct 780  
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<210> 56  
 <211> 420  
 <212> PRT  
 <213> Homo sapiens

<400> 56  
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 Gly Ser Ser Val Pro Gln Asp Gln Gln Ser Thr Asn Ile Phe Leu Ser  
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 Gln Ser Pro Met Asn Asn Leu Gln Thr Asn Thr Val Ala Gln Glu Ala  
 35 40 45  
 Phe Phe Ala Ala Pro Asn Ser Ile Ser Pro Leu Gln Ser Thr Ser Asn  
 50 55 60  
 Ser Glu Gln Gln Ala Ala Phe Gln Gln Gln Ala Pro Ile Ser His Ile  
 65 70 75 80  
 Gln Thr Pro Met Leu Ser Gln Glu Gln Ala Gln Pro Pro Gln Gln Gly  
 85 90 95  
 Leu Phe Gln Pro Gln Val Ala Leu Gly Ser Leu Pro Pro Asn Pro Met  
 100 105 110



<210> 57  
 <211> 2297  
 <212> DNA  
 <213> Homo sapiens

<400> 57  
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 ttcgtggcta ctttggggaa acaattgctc tgtactttgg atttttggag tatttcactt 180  
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 ctttccagaa tttagcctaa ttccacattt gttaaattgat gtacttataa gatcaccaat 1620  
 tgtagcactg tttgtaatat caactaaatg cccaccaata agaaaatgggt tacataaatt 1680  
 ctgatacgtc catgtaataa aatgcagaag cagtgtggca aagaatgagg gagctctttt 1740  
 agtattgaca cagaaagtcc ctcaagacac tttaaatgac taaagcaagg ggctgacag 1800  
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 atacaaactg tctggaagaa tacataagaa attgcaaata gtggttgtct tctagggaga 1920  
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 <212> PRT  
 <213> Homo sapiens

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 Val Ile Glu Ile Met Asn Arg Leu Tyr Arg Tyr Ala Ala Glu Phe Leu  
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 Arg Lys Val Gln Ala Leu Lys Ala Asp Ile Asp Ala Thr Leu Tyr Glu  
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 260 265 270  
 Asp Tyr Leu Glu Leu Phe Leu Gln Phe Gly Tyr Val Ser Leu Phe Ser  
 275 280 285  
 Cys Val Tyr Pro Leu Ala Ala Ala Phe Ala Val Leu Asn Asn Phe Thr  
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 Glu Val Asn Ser Asp Ala Leu Lys Met Cys Arg Val Phe Lys Arg Pro  
 305 310 315 320  
 Phe Ser Glu Pro Ser Ala Asn Ile Gly Val Trp Gln Met Ile Phe Cys  
 325 330 335  
 Leu Asp Thr Gly Val Lys Arg Gly Leu Asn Cys Lys Val Met Arg Asn  
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 <213> Homo sapiens

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 Thr Thr Lys Val Gln Glu Ser Leu Lys Lys Gln Glu Gly Leu Leu Lys  
 35 40 45  
 Asn Ile Gln Val Ser His Gln Glu Phe Ser Lys Met Lys Gln Ser Asn  
 50 55 60  
 Asn Glu Ala Asn Leu Arg Glu Glu Val Leu Lys Asn Leu Ala Thr Ala  
 65 70 75 80  
 Tyr Asp Asn Phe Val Glu Leu Val Ala Asn Leu Lys Glu Gly Thr Lys  
 85 90 95  
 Phe Tyr Asn Glu Leu Thr Glu Ile Leu Val Arg Phe Gln Asn Lys Cys  
 100 105 110  
 Ser Asp Ile Val Phe Ala Arg Lys Thr Glu Arg Asp Glu Leu Leu Lys  
 115 120 125  
 Asp Leu Gln Gln Ser Ile Ala Arg Glu Pro Ser Ala Pro Ser Ile Pro  
 130 135 140  
 Thr Pro Ala Tyr Gln Ser Ser Pro Ala Gly Gly His Ala Pro Thr Pro  
 145 150 155 160

Pro Thr Pro Ala Pro Arg Thr Met Pro Pro Thr Lys Pro Gln Pro Pro  
165 170 175

Ala Arg Pro Pro Pro Pro Val Leu Pro Ala Asn Arg Ala Pro Ser Ala  
180 185 190

Thr Ala Pro Ser Pro Val Gly Ala Gly Thr Ala Ala Pro Ala Pro Ser  
195 200 205

Gln Thr Pro Gly Ser Ala Pro Pro Pro Gln Ala Gln Gly Pro Pro Tyr  
210 215 220

Pro Thr Tyr Pro Gly Tyr Pro Gly Tyr Cys Gln Met Pro Met Pro Met  
225 230 235 240

Gly Tyr Asn Pro Tyr Ala Tyr Gly Gln Tyr Asn Met Pro Tyr Pro Pro  
245 250 255

Val Tyr His Gln Ser Pro Gly Gln Ala Pro Tyr Pro Gly Pro Gln Gln  
260 265 270

Pro Ser Tyr Pro Phe Pro Gln Pro Pro Gln Gln Ser Tyr Tyr Pro Gln  
275 280 285

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<210> 61  
<211> 1417  
<212> DNA  
<213> Homo sapiens

<400> 61  
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agaggttgcg accatcagtt gccaaagtaa taagagtgcg gactctgtga ttcagctact 240  
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<210> 62

<211> 414  
 <212> PRT  
 <213> Homo sapiens

<400> 62

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Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe
  35             40             45

Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys
  50             55             60

Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn
  65             70             75             80

Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg
             85             90             95

Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr
  100            105            110

Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr
  115            120            125

Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro
  130            135            140

Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu
  145            150            155            160

Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr
  165            170            175

Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val
  180            185            190

Glu Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys
  195            200            205

Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His
  210            215            220

Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln
  225            230            235            240

Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu
  245            250            255

Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys
  260            265            270

Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro
  275            280            285

Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn

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290                      295                      300  
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 Glu Glu Gly Ser Ile Arg Ala Val Asp His Ala Val Ile Gly Gly Val  
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 Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly  
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 Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys  
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 Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
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 <211> 1571  
 <212> DNA  
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 <211> 417

<212> PRT  
 <213> Homo sapiens

<400> 64

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Thr Gly Pro Arg Cys Ile Ile Pro Ser Val Ile Lys Arg Ala Gly Met
      35             40             45

Pro Lys Pro Val Arg Val Val Gln Tyr Asn Ile Asn Thr Glu Glu Leu
      50             55             60

Tyr Ser Tyr Leu Lys Glu Phe Ile His Ile Leu Tyr Phe Arg His Leu
      65             70             75             80

Leu Val Asn Pro Arg Asp Arg Arg Val Val Ile Ile Glu Ser Val Leu
      85             90             95

Cys Pro Ser His Phe Arg Glu Thr Leu Thr Arg Val Leu Phe Lys Tyr
      100            105            110

Phe Glu Val Pro Ser Val Leu Leu Ala Pro Ser His Leu Met Ala Leu
      115            120            125

Leu Thr Leu Gly Ile Asn Ser Ala Met Val Leu Asp Cys Gly Tyr Arg
      130            135            140

Glu Ser Leu Val Leu Pro Ile Tyr Glu Gly Ile Pro Val Leu Asn Cys
      145            150            155            160

Trp Gly Ala Leu Pro Leu Gly Gly Lys Ala Leu His Lys Glu Leu Glu
      165            170            175

Thr Gln Leu Leu Glu Gln Cys Thr Val Asp Thr Ser Val Ala Lys Glu
      180            185            190

Gln Ser Leu Pro Ser Val Met Gly Ser Val Pro Glu Gly Val Leu Glu
      195            200            205

Asp Ile Lys Ala Arg Thr Cys Phe Val Ser Asp Leu Lys Arg Gly Leu
      210            215            220

Lys Ile Gln Ala Ala Lys Phe Asn Ile Asp Gly Asn Asn Glu Arg Pro
      225            230            235            240

Ser Pro Pro Pro Asn Val Asp Tyr Pro Leu Asp Gly Glu Lys Ile Leu
      245            250            255

His Ile Leu Gly Ser Ile Arg Asp Ser Val Val Glu Ile Leu Phe Glu
      260            265            270

Gln Asp Asn Glu Glu Gln Ser Val Ala Thr Leu Ile Leu Asp Ser Leu
      275            280            285

Ile Gln Cys Pro Ile Asp Thr Arg Lys Gln Leu Ala Glu Asn Leu Val
      290            295            300
  
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Val Ile Gly Gly Thr Ser Met Leu Pro Gly Phe Leu His Arg Leu Leu  
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 325 330 335

Gly Thr Lys Thr Phe Arg Ile His Thr Pro Pro Ala Lys Ala Asn Cys  
 340 345 350

Val Ala Trp Leu Gly Gly Ala Ile Phe Gly Ala Leu Gln Asp Ile Leu  
 355 360 365

Gly Ser Arg Ser Val Ser Lys Glu Tyr Tyr Asn Gln Thr Gly Arg Ile  
 370 375 380

Pro Asp Trp Cys Ser Leu Asn Asn Pro Pro Leu Glu Met Met Phe Asp  
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<210> 65  
 <211> 1752  
 <212> DNA  
 <213> Homo sapiens

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 ctgacttcac ctttttgatt tgggtgtgtc cctagggtat gtacccttc ccatctgagc 1380  
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 ccagtcagtg gttctgatgt catcggttg aggtggtgt ctatacctaa aggatgacct 1500  
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gtacatttta ttgaaagga aaataaattt tttttttggg ccaaaaaaaaaa aaaaaaaaaa 1740  
 aaaaaaaaaa aa 1752

<210> 66  
 <211> 254  
 <212> PRT  
 <213> Homo sapiens

<400> 66  
 Met Tyr Gln Val Pro Leu Pro Leu Asp Arg Asp Gly Thr Leu Val Arg  
 1 5 10 15  
 Leu Arg Phe Thr Met Val Ala Leu Val Thr Val Cys Cys Pro Leu Val  
 20 25 30  
 Ala Phe Leu Phe Cys Ile Leu Trp Ser Leu Leu Phe His Phe Lys Glu  
 35 40 45  
 Thr Thr Ala Thr His Cys Gly Val Pro Asn Tyr Leu Pro Ser Val Ser  
 50 55 60  
 Ser Ala Ile Gly Gly Glu Val Pro Gln Arg Tyr Val Trp Arg Phe Cys  
 65 70 75 80  
 Ile Gly Leu His Ser Ala Pro Arg Phe Leu Val Ala Phe Ala Tyr Trp  
 85 90 95  
 Asn His Tyr Leu Ser Cys Thr Ser Pro Cys Ser Cys Tyr Arg Pro Leu  
 100 105 110  
 Cys Arg Leu Asn Phe Gly Leu Asn Val Val Glu Asn Leu Ala Leu Leu  
 115 120 125  
 Val Leu Thr Tyr Val Ser Ser Ser Glu Asp Phe Thr Ile His Glu Asn  
 130 135 140  
 Ala Phe Ile Val Phe Ile Ala Ser Ser Leu Gly His Met Leu Leu Thr  
 145 150 155 160  
 Cys Ile Leu Trp Arg Leu Thr Lys Lys His Thr Val Ser Gln Glu Asp  
 165 170 175  
 Arg Lys Ser Tyr Ser Trp Lys Gln Arg Leu Phe Ile Ile Asn Phe Ile  
 180 185 190  
 Ser Phe Phe Ser Ala Leu Ala Val Tyr Phe Arg His Asn Met Tyr Cys  
 195 200 205  
 Glu Ala Gly Val Tyr Thr Ile Phe Ala Ile Leu Glu Tyr Thr Val Val  
 210 215 220  
 Leu Thr Asn Met Ala Phe His Met Thr Ala Trp Trp Asp Phe Gly Asn  
 225 230 235 240  
 Lys Glu Leu Leu Ile Thr Ser Gln Pro Glu Glu Lys Arg Phe  
 245 250

<210> 67  
 <211> 781

<212> DNA  
 <213> Homo sapiens

<400> 67  
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 taaaaacacc agtttagtaa ccatttttat gatttggaaat accatgatgg gaacatctat 180  
 actaagcatt ccttggggca taaaacaggc tggatttact actggaatgt gtgtcatcat 240  
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 gttttcattg gataccacta cctgggaata tccagatgtc tgcagacatt atttcggctc 360  
 ctttgggcag tggtcgagtc tcctcttctc cttgggtgtc ctcattggag caatgatagt 420  
 ttattgggtg cttatgtcaa attttctttt taatactgga aagtttattt ttagtaagta 480  
 tctatatcat atgcttttaa cacagtactt tcaaatacta ttaccactgt aatgttagtt 540  
 ctagccttaa attctaggac ttgggataaa taaaataaga agtaacatat ataattttgg 600  
 aaaatatatt ttattcagtt ggctttctgt ggttgtgctc tcaaatatag tgtatgctta 660  
 tttccaaaca ttaatctttg aaggaataat attcctccaa aatccttagt taaaataaaa 720  
 tatgtctata atccaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 780  
 a 781

<210> 68  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

<400> 68  
 Met Ile Trp Asn Thr Met Met Gly Thr Ser Ile Leu Ser Ile Pro Trp  
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 Gly Ile Lys Gln Ala Gly Phe Thr Thr Gly Met Cys Val Ile Ile Leu  
 20 25 30  
 Met Gly Leu Leu Thr Leu Tyr Cys Cys Tyr Arg Val Val Lys Ser Arg  
 35 40 45  
 Thr Met Met Phe Ser Leu Asp Thr Thr Thr Trp Glu Tyr Pro Asp Val  
 50 55 60  
 Cys Arg His Tyr Phe Gly Ser Phe Gly Gln Trp Ser Ser Leu Leu Phe  
 65 70 75 80  
 Ser Leu Val Ser Leu Ile Gly Ala Met Ile Val Tyr Trp Val Leu Met  
 85 90 95  
 Ser Asn Phe Leu Phe Asn Thr Gly Lys Phe Ile Phe Ser Lys Tyr Leu  
 100 105 110  
 Tyr His Met Leu Leu Thr Gln Tyr Phe Gln Ile Leu Leu Pro Leu  
 115 120 125

<210> 69  
 <211> 649  
 <212> DNA  
 <213> Homo sapiens

<400> 69  
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 gaaccccagg ggaaggtgca atacggagag cactttcggg ttcggcagaa tctaccagag 180  
 cacacccaag gctggcttgg gagcaaatgg ctctggcttc tttttgttgt tgtgccgttt 240

gtgatactgc agtgtcaaag agacagtgcg aagaataagg agcagagtcc tcctggcctt 300  
cgaggcggcc aacttcactc tccattaaaag aaaaaaagaa atgcttcccc caacaaagac 360  
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cggaatctta aacgtgccat ggcaacaggt agtggcagta acctcaggct tcgaaagtca 480  
gagatgcctg cagatccata ccatgtcacg atctgtgaaa tatggggaga agaaagctct 540  
agctgaatgg atttgtgtgt caggagagaa aaaagttgag tgttgacaaa ctgtatgcaa 600  
actaataaaa ctattctgaa gaaaagaaaa aaaaaaaaaa aaaaaaaaaa 649

<210> 70  
<211> 171  
<212> PRT  
<213> Homo sapiens

<400> 70  
Met Trp Thr Leu Lys Ser Ser Leu Val Leu Leu Cys Leu Thr Cys  
1 5 10 15  
Ser Tyr Ala Phe Met Phe Ser Ser Leu Arg Gln Lys Thr Ser Glu Pro  
20 25 30  
Gln Gly Lys Val Gln Tyr Gly Glu His Phe Arg Ile Arg Gln Asn Leu  
35 40 45  
Pro Glu His Thr Gln Gly Trp Leu Gly Ser Lys Trp Leu Trp Leu Leu  
50 55 60  
Phe Val Val Val Pro Phe Val Ile Leu Gln Cys Gln Arg Asp Ser Glu  
65 70 75 80  
Lys Asn Lys Glu Gln Ser Pro Pro Gly Leu Arg Gly Gly Gln Leu His  
85 90 95  
Ser Pro Leu Lys Lys Lys Arg Asn Ala Ser Pro Asn Lys Asp Cys Ala  
100 105 110  
Phe Asn Thr Leu Met Glu Leu Glu Val Glu Leu Met Lys Phe Val Ser  
115 120 125  
Lys Val Arg Asn Leu Lys Arg Ala Met Ala Thr Gly Ser Gly Ser Asn  
130 135 140  
Leu Arg Leu Arg Lys Ser Glu Met Pro Ala Asp Pro Tyr His Val Thr  
145 150 155 160  
Ile Cys Glu Ile Trp Gly Glu Glu Ser Ser Ser  
165 170

<210> 71  
<211> 1456  
<212> DNA  
<213> Homo sapiens

<400> 71  
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gggtgccggg aatgctactg tctcaatgga cgggaaatgt gtgccctgat cacctgccccg 180  
gtgcctgcct gtggcaaccc caccattcac cctggacagt gctgcccacg atgtgcagat 240  
gactttgtgg tgcagaagcc agagctcagt actccctcca ttgcccacgc ccttgaggga 300  
gaatactttg tggaaggaga aacgtggaac attgactcct gtactcagtg cacctgccac 360

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agcggacggg tgctgtgtga gacagaggtg tgcccaccgc tgctctgcca gaacccctca 420
cgcacccagg attcctgctg cccacagtgt acagatcaac cttttcggcc ttccttgtcc 480
cgcaataaca gcgtacctaa ttattgcaaa aatgatgaag gggatatatt cctggcagct 540
gagtcctgga agcctgacgt ttgtaccagc tgcattctgca ttgatagcgt aattagctgt 600
ttctctgagt cctgcccttc tgtatcctgt gaaagacctg tcttgagaaa aggcagtggt 660
tgtccctact gcatagaaga cacaattcca aagaaggtgg tgtgccactt cagtgggaag 720
gcctatgccg acgaggagcg gtgggacctt gacagctgca cccactgcta ctgcctgcag 780
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<210> 72
<211> 400
<212> PRT
<213> Homo sapiens

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<400> 72
Met Cys Ala Leu Ile Thr Cys Pro Val Pro Ala Cys Gly Asn Pro Thr
  1                      5                      10                      15

Ile His Pro Gly Gln Cys Cys Pro Ser Cys Ala Asp Asp Phe Val Val
                20                      25                      30

Gln Lys Pro Glu Leu Ser Thr Pro Ser Ile Cys His Ala Pro Gly Gly
    35                      40                      45

Glu Tyr Phe Val Glu Gly Glu Thr Trp Asn Ile Asp Ser Cys Thr Gln
    50                      55                      60

Cys Thr Cys His Ser Gly Arg Val Leu Cys Glu Thr Glu Val Cys Pro
    65                      70                      75                      80

Pro Leu Leu Cys Gln Asn Pro Ser Arg Thr Gln Asp Ser Cys Cys Pro
                85                      90                      95

Gln Cys Thr Asp Gln Pro Phe Arg Pro Ser Leu Ser Arg Asn Asn Ser
    100                      105                      110

Val Pro Asn Tyr Cys Lys Asn Asp Glu Gly Asp Ile Phe Leu Ala Ala
    115                      120                      125

Glu Ser Trp Lys Pro Asp Val Cys Thr Ser Cys Ile Cys Ile Asp Ser
    130                      135                      140

Val Ile Ser Cys Phe Ser Glu Ser Cys Pro Ser Val Ser Cys Glu Arg
    145                      150                      155                      160

Pro Val Leu Arg Lys Gly Gln Cys Cys Pro Tyr Cys Ile Glu Asp Thr
                165                      170                      175

Ile Pro Lys Lys Val Val Cys His Phe Ser Gly Lys Ala Tyr Ala Asp

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180	185	190
Glu Glu Arg Trp Asp Leu Asp Ser Cys Thr His Cys Tyr Cys Leu Gln 195 200 205		
Gly Gln Thr Leu Cys Ser Thr Val Ser Cys Pro Pro Leu Pro Cys Val 210 215 220		
Glu Pro Ile Asn Val Glu Gly Ser Cys Cys Pro Met Cys Pro Glu Met 225 230 235 240		
Tyr Val Pro Glu Pro Thr Asn Ile Pro Ile Glu Lys Thr Asn His Arg 245 250 255		
Gly Glu Val Asp Leu Glu Val Pro Leu Trp Pro Thr Pro Ser Glu Asn 260 265 270		
Asp Ile Val His Leu Pro Arg Asp Met Gly His Leu Gln Val Asp Tyr 275 280 285		
Arg Asp Asn Arg Leu His Pro Ser Glu Asp Ser Ser Leu Asp Ser Ile 290 295 300		
Ala Ser Val Val Val Pro Ile Ile Ile Cys Leu Ser Ile Ile Ile Ala 305 310 315 320		
Phe Leu Phe Ile Asn Gln Lys Lys Gln Trp Ile Pro Leu Leu Cys Trp 325 330 335		
Tyr Arg Thr Pro Thr Lys Pro Ser Ser Leu Asn Asn Gln Leu Val Ser 340 345 350		
Val Asp Cys Lys Lys Gly Thr Arg Val Gln Val Asp Ser Ser Gln Arg 355 360 365		
Met Leu Arg Ile Ala Glu Pro Asp Ala Arg Phe Ser Gly Phe Tyr Ser 370 375 380		
Met Gln Lys Gln Asn His Leu Gln Ala Asp Asn Phe Tyr Gln Thr Val 385 390 395 400		

<210> 73  
 <211> 4723  
 <212> DNA  
 <213> Homo sapiens

<400> 73  
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 ggatgctact cgggcaccta gaagccacag ctgccctcca cagagcggca ctgcaccatg 180  
 cgcaggaatg tctcgacctt gtccatgtcc ttcttgaagc agtagagcag cccgtagttc 240  
 ttgagcagtg cgctcatggtt gtgcgagttt gtgtcaaact tgctgtaggt ctgcttgagg 300  
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 tctaggtcct ttagggagtg atagtcacg ttgtccgagg tgcatacac cagggtgttg 420  
 gcgaacatac tcctgaggaa cgcacgggc tccagccacg actcgatgag cagcagggag 480  
 atgcggagca gctctagatt ggatttctgt tgcgtttcct ccatgttgga ggggtgtcga 540  
 atagagtctg agaagcagaa ggaggtcttg gagtcacgca ggaatgaata cttctgggtc 600  
 tttgggatat aggtttcttc aaactcctgg taggtgtcaa tggccagctg gtgcgcgcga 660  
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<210> 74  
 <211> 1036  
 <212> PRT  
 <213> Homo sapiens

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<400> 74
Met Tyr Leu Val Ala Gly Asp Arg Gly Leu Ala Gly Cys Gly His Leu
  1             5             10            15

Leu Val Ser Leu Leu Gly Leu Leu Leu Leu Leu Ala Arg Ser Gly Thr
      20             25             30

Arg Ala Leu Val Cys Leu Pro Cys Asp Glu Ser Lys Cys Glu Glu Pro
      35             40             45

Arg Asn Cys Pro Gly Ser Ile Val Gln Gly Val Cys Gly Cys Cys Tyr
      50             55             60

Thr Cys Ala Ser Gln Arg Asn Glu Ser Cys Gly Gly Thr Phe Gly Ile
      65             70             75             80

Tyr Gly Thr Cys Asp Arg Gly Leu Arg Cys Val Ile Arg Pro Pro Leu
      85             90             95

Asn Gly Asp Ser Leu Thr Glu Tyr Glu Ala Gly Val Cys Glu Asp Glu
      100            105            110

Asn Trp Thr Asp Asp Gln Leu Leu Gly Phe Lys Pro Cys Asn Glu Asn
      115            120            125

Leu Ile Ala Gly Cys Asn Ile Ile Asn Gly Lys Cys Glu Cys Asn Thr
      130            135            140

Ile Arg Thr Cys Ser Asn Pro Phe Glu Phe Pro Ser Gln Asp Met Cys
      145            150            155            160

Leu Ser Ala Leu Lys Arg Ile Glu Glu Glu Lys Pro Asp Cys Ser Lys
      165            170            175

Ala Arg Cys Glu Val Gln Phe Ser Pro Arg Cys Pro Glu Asp Ser Val
      180            185            190

Leu Ile Glu Gly Tyr Ala Pro Pro Gly Glu Cys Cys Pro Leu Pro Ser
      195            200            205

Arg Cys Val Cys Asn Pro Ala Gly Cys Leu Arg Lys Val Cys Gln Pro
      210            215            220

Gly Asn Leu Asn Ile Leu Val Ser Lys Ala Ser Gly Lys Pro Gly Glu
      225            230            235            240

Cys Cys Asp Leu Tyr Glu Cys Lys Pro Val Phe Gly Val Asp Cys Arg

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885	890	895
Leu Glu Val Pro Leu Trp Pro Thr Pro Ser Glu Asn Asp Ile Val His 900 905 910		
Leu Pro Arg Asp Met Gly His Leu Gln Val Asp Tyr Arg Asp Asn Arg 915 920 925		
Leu His Pro Ser Glu Asp Ser Ser Leu Asp Ser Ile Ala Ser Val Val 930 935 940		
Val Pro Ile Ile Ile Cys Leu Ser Ile Ile Ile Ala Phe Leu Phe Ile 945 950 955 960		
Asn Gln Lys Lys Gln Trp Ile Pro Leu Leu Cys Trp Tyr Arg Thr Pro 965 970 975		
Thr Lys Pro Ser Ser Leu Asn Asn Gln Leu Val Ser Val Asp Cys Lys 980 985 990		
Lys Gly Thr Arg Val Gln Val Asp Ser Ser Gln Arg Met Leu Arg Ile 995 1000 1005		
Ala Glu Pro Asp Ala Arg Phe Ser Gly Phe Tyr Ser Met Gln Lys Gln 1010 1015 1020		
Asn His Leu Gln Ala Asp Asn Phe Tyr Gln Thr Val 1025 1030 1035		

<210> 75  
 <211> 3861  
 <212> DNA  
 <213> Homo sapiens

<400> 75  
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<210> 76  
 <211> 457  
 <212> PRT  
 <213> Homo sapiens

<400> 76  
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 Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu  
 35 40 45  
 Arg Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn  
 50 55 60

Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys  
 65 70 75 80  
 Pro Asn Val His Cys Leu Ser Pro Val His Ile Pro His Leu Cys Cys  
 85 90 95  
 Pro Arg Cys Pro Asp Ser Leu Pro Pro Val Asn Asn Lys Val Thr Ser  
 100 105 110  
 Lys Ser Cys Glu Tyr Asn Gly Thr Thr Tyr Gln His Gly Glu Leu Phe  
 115 120 125  
 Val Ala Glu Gly Leu Phe Gln Asn Arg Gln Pro Asn Gln Cys Thr Gln  
 130 135 140  
 Cys Ser Cys Ser Glu Gly Asn Val Tyr Cys Gly Leu Lys Thr Cys Pro  
 145 150 155 160  
 Lys Leu Thr Cys Ala Phe Pro Val Ser Val Pro Asp Ser Cys Cys Arg  
 165 170 175  
 Val Cys Arg Gly Asp Gly Glu Leu Ser Trp Glu His Ser Asp Gly Asp  
 180 185 190  
 Ile Phe Arg Gln Pro Ala Asn Arg Glu Ala Arg His Ser Tyr His Arg  
 195 200 205  
 Ser His Tyr Asp Pro Pro Pro Ser Arg Gln Ala Gly Gly Leu Ser Arg  
 210 215 220  
 Phe Pro Gly Ala Arg Ser His Arg Gly Ala Leu Met Asp Ser Gln Gln  
 225 230 235 240  
 Ala Ser Gly Thr Ile Val Gln Ile Val Ile Asn Asn Lys His Lys His  
 245 250 255  
 Gly Gln Val Cys Val Ser Asn Gly Lys Thr Tyr Ser His Gly Glu Ser  
 260 265 270  
 Trp His Pro Asn Leu Arg Ala Phe Gly Ile Val Glu Cys Val Leu Cys  
 275 280 285  
 Thr Cys Asn Val Thr Lys Gln Glu Cys Lys Lys Ile His Cys Pro Asn  
 290 295 300  
 Arg Tyr Pro Cys Lys Tyr Pro Gln Lys Ile Asp Gly Lys Cys Cys Lys  
 305 310 315 320  
 Val Cys Pro Gly Lys Lys Ala Lys Glu Glu Leu Pro Gly Gln Ser Phe  
 325 330 335  
 Asp Asn Lys Gly Tyr Phe Cys Gly Glu Glu Thr Met Pro Val Tyr Glu  
 340 345 350  
 Ser Val Phe Met Glu Asp Gly Glu Thr Thr Arg Lys Ile Ala Leu Glu  
 355 360 365  
 Thr Glu Arg Pro Pro Gln Val Glu Val His Val Trp Thr Ile Arg Lys  
 370 375 380

Gly Ile Leu Gln His Phe His Ile Glu Lys Ile Ser Lys Arg Met Phe  
 385 390 395 400

Glu Glu Leu Pro His Phe Lys Leu Val Thr Arg Thr Thr Leu Ser Gln  
 405 410 415

Trp Lys Ile Phe Thr Glu Gly Glu Ala Gln Ile Ser Gln Met Cys Ser  
 420 425 430

Ser Arg Val Cys Arg Thr Glu Leu Glu Asp Leu Val Lys Val Leu Tyr  
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Leu Glu Arg Ser Glu Lys Gly His Cys  
 450 455

<210> 77  
 <211> 2050  
 <212> DNA  
 <213> Homo sapiens

<400> 77  
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 agattgatct tcttcacacc aagctctgtt tacattccga gaggtgtcat gaagaaagtt 1980  
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<210> 78  
 <211> 505

<212> PRT  
 <213> Homo sapiens

<400> 78

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Lys Asn Cys Trp Arg Ile Lys Lys Gly Phe Val Pro Asn Met Gln Val
 20           25           30

Glu Gly Val Phe Tyr Val Asn Asp Ala Leu Glu Lys Leu Met Phe Glu
 35           40           45

Glu Leu Arg Asn Ala Cys Arg Gly Gly Gly Val Gly Gly Phe Leu Pro
 50           55           60

Ala Met Lys Gln Ile Gly Asn Val Ala Ala Leu Pro Gly Ile Val His
 65           70           75           80

Arg Ser Ile Gly Leu Pro Asp Val His Ser Gly Tyr Gly Phe Ala Ile
 85           90           95

Gly Asn Met Ala Ala Phe Asp Met Asn Asp Pro Glu Ala Val Val Ser
 100          105          110

Pro Gly Gly Val Gly Phe Asp Ile Asn Cys Gly Val Arg Leu Leu Arg
 115          120          125

Thr Asn Leu Asp Glu Ser Asp Val Gln Pro Val Lys Glu Gln Leu Ala
 130          135          140

Gln Ala Met Phe Asp His Ile Pro Val Gly Val Gly Ser Lys Gly Val
 145          150          155          160

Ile Pro Met Asn Ala Lys Asp Leu Glu Glu Ala Leu Glu Met Gly Val
 165          170          175

Asp Trp Ser Leu Arg Glu Gly Tyr Ala Trp Ala Glu Asp Lys Glu His
 180          185          190

Cys Glu Glu Tyr Gly Arg Met Leu Gln Ala Asp Pro Asn Lys Val Ser
 195          200          205

Ala Arg Ala Lys Lys Arg Gly Leu Pro Gln Leu Gly Thr Leu Gly Ala
 210          215          220

Gly Asn His Tyr Ala Glu Ile Gln Val Val Asp Glu Ile Phe Asn Glu
 225          230          235          240

Tyr Ala Ala Lys Lys Met Gly Ile Asp His Lys Gly Gln Val Cys Val
 245          250          255

Met Ile His Ser Gly Ser Arg Gly Leu Gly His Gln Val Ala Thr Asp
 260          265          270

Ala Leu Val Ala Met Glu Lys Ala Met Lys Arg Asp Lys Ile Ile Val
 275          280          285

Asn Asp Arg Gln Leu Ala Cys Ala Arg Ile Ala Ser Pro Glu Gly Gln
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Asp Tyr Leu Lys Gly Met Ala Ala Ala Gly Asn Tyr Ala Trp Val Asn  
 305 310 315 320  
 Arg Ser Ser Met Thr Phe Leu Thr Arg Gln Ala Phe Ala Lys Val Phe  
 325 330 335  
 Asn Thr Thr Pro Asp Asp Leu Asp Leu His Val Ile Tyr Asp Val Ser  
 340 345 350  
 His Asn Ile Ala Lys Val Glu Gln His Val Val Asp Gly Lys Glu Arg  
 355 360 365  
 Thr Leu Leu Val His Arg Lys Gly Ser Thr Arg Ala Phe Pro Pro His  
 370 375 380  
 His Pro Leu Ile Ala Val Asp Tyr Gln Leu Thr Gly Gln Pro Val Leu  
 385 390 395 400  
 Ile Gly Gly Thr Met Gly Thr Cys Ser Tyr Val Leu Thr Gly Thr Glu  
 405 410 415  
 Gln Gly Met Thr Glu Thr Phe Gly Thr Thr Cys His Gly Ala Gly Arg  
 420 425 430  
 Ala Leu Ser Arg Ala Lys Ser Arg Arg Asn Leu Asp Phe Gln Asp Val  
 435 440 445  
 Leu Asp Lys Leu Ala Asp Met Gly Ile Ala Ile Arg Val Ala Ser Pro  
 450 455 460  
 Lys Leu Val Met Glu Glu Ala Pro Glu Ser Tyr Lys Asn Val Thr Asp  
 465 470 475 480  
 Val Val Asn Thr Cys His Asp Ala Gly Ile Ser Lys Lys Ala Ile Lys  
 485 490 495  
 Leu Arg Pro Ile Ala Val Ile Lys Gly  
 500 505

<210> 79  
 <211> 1178  
 <212> DNA  
 <213> Homo sapiens

<400> 79  
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 aagggtgtaa aacatcgacc cccaccaatc aaacttccct caagctcagg aaatagttcc 180  
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<210> 80  
 <211> 310  
 <212> PRT  
 <213> Homo sapiens

<400> 80  
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 20 25 30  
 Leu Gly Lys Gly Val Lys His Arg Pro Pro Pro Ile Lys Leu Pro Ser  
 35 40 45  
 Ser Ser Gly Asn Ser Ser Ser Gly Asn Tyr Phe Thr Pro Gln Gln Thr  
 50 55 60  
 Ser Ser Phe Leu Lys Ser Pro Thr Pro Pro Pro Ser Ser Lys Pro Ser  
 65 70 75 80  
 Ser Ile Pro Arg Lys Ser Ser Val Asp Leu Asn Gln Val Ser Met Leu  
 85 90 95  
 Ser Pro Ala Ala Leu Ser Pro Ala Ser Ser Ser Gln Arg Thr Thr Ala  
 100 105 110  
 Thr Gln Val Met Ala Asn Ser Ala Gly Leu Asn Phe Ile Asn Val Val  
 115 120 125  
 Gly Ser Val Cys Gly Ala Gln Ala Leu Met Ser Gly Ser Asn Pro Met  
 130 135 140  
 Leu Gly Cys Asn Thr Gly Ala Ile Thr Pro Ala Gly Ile Asn Leu Ser  
 145 150 155 160  
 Gly Leu Leu Pro Ser Gly Gly Leu Leu Pro Asn Ala Leu Pro Ser Ala  
 165 170 175  
 Met Gln Ala Ala Ser Gln Ala Gly Val Pro Phe Gly Leu Lys Asn Thr  
 180 185 190  
 Ser Ser Leu Arg Pro Leu Asn Leu Leu Gln Leu Pro Gly Gly Ser Leu  
 195 200 205  
 Ile Phe Asn Thr Leu Gln Gln Gln Gln Gln Gln Leu Ser Gln Phe Thr  
 210 215 220  
 Pro Gln Gln Pro Gln Gln Pro Thr Thr Cys Ser Pro Gln Gln Pro Gly  
 225 230 235 240  
 Glu Gln Gly Ser Glu Gln Gly Ser Thr Ser Gln Glu Gln Ala Leu Ser



245 250 255  
 Ala Gln Gln Ala Ala Val Ile Asn Leu Thr Gly Val Gly Ser Phe Met  
 260 265 270  
 Gln Ser Gln Ala Ala Ala Val Ala Ile Leu Ala Ala Ser Asn Gly Tyr  
 275 280 285  
 Gly Ser Ser Ser Ser Thr Asn Ser Ser Ala Thr Ser Ser Ser Ala Tyr  
 290 295 300  
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 305 310

<210> 81  
 <211> 641  
 <212> DNA  
 <213> Homo sapiens

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 cctggatgtt gtcactagtc tagtggcttt tgctaaataa acctttctta tttctaaaaa 540  
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<210> 82  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<400> 82  
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 Trp Thr Pro Gly Val Leu Thr Leu Leu Val Pro Ala Pro Ala Tyr Pro  
 35 40 45  
 Arg Cys Gln Gln Thr Leu Val His Arg Arg Leu Pro Gln Leu Trp Ser  
 50 55 60  
 Gln Glu Arg Ile Ser Leu His Trp Met Asp Cys Ile Leu Arg Leu Lys  
 65 70 75 80  
 Ile Ile Phe Leu Ile Phe Leu Leu Ile Ser Met Leu Ser Leu  
 85 90

<210> 83  
 <211> 832

<212> DNA  
 <213> Homo sapiens

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 tgtcatgaga ggaagaaaca agaatgacaa gtgtatgact gcctttgagc tgtagtcccc 780  
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<210> 84  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
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 35 40 45  
 Arg Tyr Phe Leu Ile Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr  
 50 55 60  
 Val Ala Ile Val Ser Thr Thr Phe Leu Val His Leu Val Val Met Ser  
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<210> 92  
 <211> 392  
 <212> PRT  
 <213> Homo sapiens

<400> 92  
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Tyr	Arg	Ile	Ala	Arg	Arg	Met	Lys	Pro	Thr	His	Thr	Met	Val	Asn	Cys
35								40				45			
Trp	Phe	Cys	Asn	Gln	Asp	Thr	Leu	Val	Pro	Tyr	Gly	Asn	Arg	Asn	Cys
50								55				60			
Trp	Asp	Cys	Pro	His	Cys	Glu	Gln	Tyr	Asn	Gly	Phe	Gln	Glu	Asn	Gly
65								70				75			
Asp	Tyr	Asn	Lys	Pro	Ile	Pro	Ala	Gln	Tyr	Leu	Glu	His	Leu	Asn	His
				85								90			
Val	Val	Ser	Ser	Ala	Pro	Ser	Leu	Arg	Asp	Pro	Ser	Gln	Pro	Gln	Gln
100								105				110			
Trp	Val	Ser	Ser	Gln	Val	Leu	Leu	Cys	Lys	Arg	Cys	Asn	His	His	Gln
115								120				125			
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180								185				190			
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Lys	Ser	Pro	Val	Gln	Val	Ile	Leu	Leu	Arg	Ala	Leu	Ala	Phe	Leu	Ala
210								215				220			
Cys	Ala	Phe	Leu	Leu	Thr	Thr	Ala	Leu	Tyr	Gly	Ala	Ser	Gly	His	Phe
225								230				235			
Ala	Pro	Gly	Thr	Thr	Val	Pro	Leu	Ala	Leu	Pro	Pro	Gly	Gly	Asn	Gly
				245								250			
Ser	Ala	Thr	Pro	Asp	Asn	Gly	Thr	Thr	Pro	Gly	Ala	Glu	Gly	Trp	Arg
260								265				270			
Gln	Leu	Leu	Gly	Leu	Leu	Pro	Glu	His	Met	Ala	Glu	Lys	Leu	Cys	Glu
275								280				285			
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290								295				300			
Leu	Leu	Thr	Cys	Leu	Leu	Ala	Met	Leu	Leu	Ala	Gly	Arg	Ile	Arg	Leu
305								310				315			
Arg	Arg	Ile	Asp	Ala	Phe	Cys	Thr	Cys	Leu	Trp	Ala	Leu	Leu	Leu	Gly
				325								330			

Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro Ser Trp Leu  
 340 345 350  
 Asn Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu Val Gly Phe  
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 Thr Ala Ala Val Ala Thr Arg Lys Ala Thr Gly Pro Arg Arg Phe Arg  
 370 375 380  
 Pro Arg Arg Ser Glu Lys Gln Pro  
 385 390

<210> 93  
 <211> 2203  
 <212> DNA  
 <213> Homo sapiens

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<210> 94  
 <211> 674  
 <212> PRT

<213> Homo sapiens

<400> 94

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35 40 45  
Lys Val His Leu Asp Ser Ala Val Ala Leu Ala Ala Glu Ser Pro Val  
50 55 60  
Asn Met Met Pro Trp Gln Gly Asp Thr Asn Asn Met Ile Asp Arg Phe  
65 70 75 80  
Asp Val Arg Ala His Leu Asp His Ile Pro Asp Tyr Thr Pro Pro Leu  
85 90 95  
Leu Thr Thr Ile Ser Pro Glu Gln Glu Ser Asp Glu Arg Lys Cys Asn  
100 105 110  
Tyr Glu Arg Tyr Arg Gly Leu Val Gln Asn Asp Phe Ala Gly Ile Ser  
115 120 125  
Glu Glu Gln Cys Leu Tyr Gln Ile Tyr Ile Asp Glu Leu Tyr Gly Gly  
130 135 140  
Leu Gln Arg Pro Ser Glu Asp Glu Lys Lys Lys Leu Ala Glu Lys Lys  
145 150 155 160  
Ala Ser Ile Gly Tyr Thr Tyr Glu Asp Ser Thr Val Ala Glu Val Glu  
165 170 175  
Lys Ala Ala Glu Lys Pro Glu Glu Glu Glu Ser Ala Ala Glu Glu Glu  
180 185 190  
Ser Asn Ser Asp Glu Asp Glu Val Ile Pro Asp Ile Asp Val Glu Val  
195 200 205  
Asp Val Asp Glu Leu Asn Gln Glu Gln Val Ala Asp Leu Asn Lys Gln  
210 215 220  
Ala Thr Thr Tyr Gly Met Ala Asp Gly Asp Phe Val Arg Met Leu Arg  
225 230 235 240  
Lys Asp Lys Glu Glu Ala Glu Ala Ile Lys His Ala Lys Ala Leu Glu  
245 250 255  
Glu Glu Lys Ala Met Tyr Ser Gly Arg Arg Ser Arg Arg Gln Arg Arg  
260 265 270  
Glu Phe Arg Glu Lys Arg Leu Arg Gly Arg Lys Ile Ser Pro Pro Ser  
275 280 285  
Tyr Ala Arg Arg Asp Ser Pro Thr Tyr Asp Pro Tyr Lys Arg Ser Pro  
290 295 300

Ser Glu Ser Ser Ser Glu Ser Arg Ser Arg Ser Arg Ser Pro Thr Pro  
305 310 315 320

Gly Arg Glu Glu Lys Ile Thr Phe Ile Thr Ser Phe Gly Gly Ser Asp  
325 330 335

Glu Glu Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ser Gly Val Thr  
340 345 350

Thr Gly Lys Pro Pro Ala Pro Pro Gln Pro Gly Gly Pro Ala Pro Gly  
355 360 365

Arg Asn Ala Ser Ala Arg Arg Arg Ser Ser Ser Ser Ser Ser Ser Ser  
370 375 380

Ser Ala Ser Arg Thr Ser Ser Ser Arg Ser Ser Ser Arg Ser Ser Ser  
385 390 395 400

Arg Ser Arg Arg Gly Gly Gly Tyr Tyr Arg Ser Gly Arg His Ala Arg  
405 410 415

Ser Arg Ser Arg Ser Trp Ser Arg Ser Arg Ser Arg Ser Arg Arg Tyr  
420 425 430

Ser Arg Ser Arg Ser Arg Gly Arg Arg His Ser Gly Gly Gly Ser Arg  
435 440 445

Asp Gly His Arg Tyr Ser Arg Ser Pro Ala Arg Arg Gly Gly Tyr Gly  
450 455 460

Pro Arg Arg Arg Ser Arg Ser Arg Ser His Ser Gly Asp Arg Tyr Arg  
465 470 475 480

Arg Gly Gly Arg Gly Leu Arg His His Ser Ser Ser Arg Ser Arg Ser  
485 490 495

Ser Trp Ser Leu Ser Pro Ser Arg Ser Arg Ser Leu Thr Arg Ser Arg  
500 505 510

Ser His Ser Pro Ser Pro Ser Gln Ser Arg Ser Arg Ser Arg Ser Arg  
515 520 525

Ser Gln Ser Pro Ser Pro Ser Pro Ala Arg Glu Lys Leu Thr Arg Pro  
530 535 540

Ala Ala Ser Pro Ala Val Gly Glu Lys Leu Lys Lys Thr Glu Pro Ala  
545 550 555 560

Ala Gly Lys Glu Thr Gly Ala Ala Lys Pro Lys Leu Thr Pro Gln Glu  
565 570 575

Lys Leu Lys Leu Arg Met Gln Lys Ala Leu Asn Arg Gln Phe Lys Ala  
580 585 590

Asp Lys Lys Ala Ala Gln Glu Lys Met Ile Gln Gln Glu His Glu Arg  
595 600 605

Gln Glu Arg Glu Asp Glu Leu Arg Ala Met Ala Arg Lys Ile Arg Met  
610 615 620

Lys Glu Arg Glu Arg Arg Glu Lys Glu Arg Glu Glu Trp Glu Arg Gln  
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Tyr Ser Arg Gln Ser Arg Ser Pro Ser Pro Arg Tyr Ser Arg Glu Tyr  
645 650 655

Ser Ser Ser Arg Arg Arg Ser Arg Ser Arg Ser Arg Ser Pro His Tyr  
660 665 670

Arg His

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<211> 1014  
<212> DNA  
<213> Homo sapiens

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<210> 96  
<211> 204  
<212> PRT  
<213> Homo sapiens

<400> 96  
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Ser Phe Ile Lys Trp Cys Asn Ser Gly Ser Gln Glu Glu Gly Tyr Ser  
35 40 45  
Gln Tyr Gln Arg Met Leu Ser Thr Leu Ser Gln Cys Glu Phe Ser Met  
50 55 60  
Gly Lys Thr Leu Leu Val Tyr Asp Met Asn Leu Arg Glu Met Glu Asn  
65 70 75 80  
Tyr Glu Lys Ile Tyr Lys Glu Ile Glu Cys Ser Ile Ala Gly Ala His  
85 90 95

Glu Lys Ile Ala Glu Cys Lys Lys Gln Ile Leu Gln Ala Lys Arg Ile  
 100 105 110  
 Arg Lys Asn Arg Gln Glu Tyr Asp Ala Leu Ala Lys Val Ile Gln His  
 115 120 125  
 His Pro Asp Arg His Glu Thr Leu Lys Glu Leu Glu Ala Leu Gly Lys  
 130 135 140  
 Glu Leu Glu His Leu Ser His Ile Lys Glu Ser Val Glu Asp Lys Leu  
 145 150 155 160  
 Glu Leu Arg Arg Lys Gln Phe His Val Leu Leu Ser Thr Ile His Glu  
 165 170 175  
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<210> 97  
 <211> 955  
 <212> DNA  
 <213> Homo sapiens

<400> 97  
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 ccattcaagg acagtggaaa tatttcttta aatgatttca ttttcttta gaccgattat 780  
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<210> 98  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 98  
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 Asp Ile Glu Glu Lys Lys Ser Ile Lys Lys Lys Ile Lys Glu Leu Lys  
 35 40 45



Phe Leu Asp Ser Lys Ile Ala Gln Asn Leu Cys Lys Tyr His Ile Pro  
50 55 60

Ile Pro Phe Lys Asp Ser Gly Asn Ile Ser Leu Asn Asp Phe Ile Phe  
65 70 75 80

Phe Lys Thr Asp Tyr Ser Leu Phe Ala Ile Phe Ile Leu Leu Leu Tyr  
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Ala

<210> 99  
<211> 1375  
<212> DNA  
<213> Homo sapiens

<400> 99  
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<210> 100  
<211> 132  
<212> PRT  
<213> Homo sapiens

<400> 100  
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20 25 30  
Cys Arg Gly Ser Trp Gln Leu Leu Gly Glu Val Ser Trp His Arg Leu  
35 40 45  
Thr Leu Leu Ser Gly Thr Thr Ser Phe Pro Phe Glu Glu Thr Ala Thr

50 55 60

Ala Val Ala Lys Ala Ala Ala Ala Pro Ala Met Arg Val Tyr Ile Phe  
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Gly Lys Glu Pro Cys Ile Ile Cys Glu His Cys Ile Ile Gly Asn Val  
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Pro Leu Trp Thr  
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Pro Val Leu Ser Thr Gly Thr Ala Val Ser Glu Leu Leu Arg Thr Ser  
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Leu Cys Gln Val Val Glu Leu Gly Pro Ser Pro Tyr Leu Ser Leu Val  
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Trp Arg Pro Trp  
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<212> DNA

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<213> Homo sapiens

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Tyr Glu Phe Glu Ile Thr Asp Leu Phe Ser Ser Tyr Cys Ile His Ile  
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Asn Ile Cys Glu Phe Val Val Gln Leu Phe Ile Gln Thr Lys Asn Ile  
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Pro Ser Arg Lys Leu His Phe Tyr His Lys His Phe Asn Ile Thr Asn  
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Ile Arg Thr Ser Leu Pro Cys

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Ala Pro Glu Ser Ser Lys Lys Arg Ala Arg Arg Met Arg Pro Asp Leu  
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Ser Lys Met Met Ala Leu Met Gln Gly Gly Ser Thr Gly Ser Leu Ser  
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Leu His Asn Thr Phe Gln His Ser Ser Ser Gly Leu Gln Ser Val Ser  
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Ser Leu Gly His Ser Ser Ala Thr Ser Ala Ser Leu Pro Phe Met Pro  
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His His Pro Gly Leu Arg Ala Pro Gly Tyr Pro Ser Ser Pro Val Thr  
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<211> 3004

<212> DNA

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<212> PRT

<213> Homo sapiens

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Leu Val Lys Glu Ala Gln Pro Leu Val Trp Val Lys Asp Pro Leu Gln  
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Leu Thr Ser Asn Pro Leu Gly Pro Pro Glu Pro Trp Ser Ser Arg Ser  
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Ser His Leu Pro Trp Glu Ser Pro His Ala Pro Ala Pro Pro Ala Ala  
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Pro Gly Asp Phe Asp Tyr Leu Gly Pro Ser Ala Ser Ser Gln Met Ser





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His Val Ile Arg Thr Leu Lys Met Glu Cys Ser Glu Thr His Val Gln					
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Asp Gln Gln Lys Thr Asn Tyr Ile Asn Glu Asn Met Glu Gln Asn Glu					
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Gln Lys Glu Gln Lys Ser Ser Glu Leu Met Lys Glu Val Pro Gly Asp					
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Asp Tyr Lys Asn Lys Leu Ile Phe Ala Ile Ser Val Thr Val Ile Leu					
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<211> 1331

<212> DNA

<213> Homo sapiens

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<212> PRT  
<213> Homo sapiens

<400> 110  
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20 25 30  
Gly Gly Glu Val Ala Tyr Gly Gln Val Leu Gly Val Ile Gly Tyr Ser  
35 40 45  
Leu Leu Pro Leu Ile Val Ile Ala Pro Val Leu Leu Val Val Gly Ser  
50 55 60  
Phe Glu Val Val Ser Thr Leu Ile Lys Leu Phe Gly Val Phe Trp Ala  
65 70 75 80  
Ala Tyr Ser Ala Ala Ser Leu Leu Val Gly Glu Glu Phe Lys Thr Lys  
85 90 95  
Lys Pro Leu Leu Ile Tyr Pro Ile Phe Leu Leu Tyr Ile Tyr Phe Leu  
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Ser Leu Tyr Thr Gly Val  
115

<210> 111  
<211> 2610  
<212> DNA  
<213> Homo sapiens

<400> 111  
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agccctttg ctatgatcaa ctgcaaagga aagaaactaa atatggttca gtgataaaca 540
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<210> 112  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 112  
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 Leu Ser Leu Tyr Thr His Val Thr Cys Ser Ser Leu Pro Ser Ser Leu  
                     20                    25                    30  
 Cys Leu Tyr Ile Tyr Tyr Tyr His Arg Gly Leu Gly Lys Lys Thr Pro  
                     35                    40                    45  
 Thr Ala Ala Pro His Thr His Pro Pro Ala Leu Tyr His Leu Leu Cys  
                     50                    55                    60  
 Phe Val Phe Leu Cys Arg Ile His Asp Phe Leu Lys Tyr Asn Phe Phe  
                     65                    70                    75                    80  
 Asn Val Tyr Ile Leu Tyr Ala Phe Ser His Ser Tyr Val Lys Ser Gly  
                     85                    90                    95

Arg His Arg Leu Val Phe Leu Phe Thr Val Asp Ala Ser Val Pro Lys  
 100 105 110

Ile Cys Ile Ala  
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<210> 113  
 <211> 2759  
 <212> DNA  
 <213> Homo sapiens

<400> 113  
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 ggacatgtgc cggccgcaag tgctcaggcc cagcaaggcg tctgtccacc gcaggccgtg 720  
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<210> 114  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 114  
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           20                  25                  30  
  
 Cys Thr Asp Thr Glu Cys Leu Gln Glu Leu Pro Gly Pro Ser Gly Asp  
           35                  40                  45  
  
 Asn Gly Ile Ser Val Thr Met Ile Leu Val Ala Trp Met Val Ile Ala  
   50                  55                  60  
  
 Leu Ile Leu Phe Leu Leu Arg Pro Pro Asn Leu Arg Gly Ser Ser Leu  
   65                  70                  75                  80  
  
 Pro Gly Lys Pro Thr Ser Pro His Asn Gly Gln Asp Pro Pro Ala Pro  
           85                  90                  95  
  
 Pro Val Asp

<210> 115  
 <211> 1404  
 <212> DNA  
 <213> Homo sapiens

<400> 115  
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 gatgagattt agggtttcc cggggccttc gggatcttca cctaataatcc ggtattattt 300  
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 tcttcagaaa aaaaaaaaaa aaaa 1404

<210> 116  
 <211> 184  
 <212> PRT  
 <213> Homo sapiens

<400> 116  
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                   20                  25                  30  
  
 Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys Leu  
           35                  40                  45  
  
 Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys Ala Phe Ile Asn Leu  
           50                  55                  60  
  
 Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp Glu  
           65                  70                  75                  80  
  
 Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr Val  
                   85                  90                  95  
  
 Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala Leu  
           100                  105                  110  
  
 Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly Ser  
           115                  120                  125  
  
 His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro Lys  
           130                  135                  140  
  
 Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser Ser  
           145                  150                  155                  160  
  
 Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala Gly  
                   165                  170                  175  
  
 Leu Ala Leu Glu Ile Arg Ser Leu  
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<210> 117  
 <211> 1801  
 <212> DNA  
 <213> Homo sapiens

<400> 117  
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 tatgtatctg gacaaattac ttcaattgct tgacagtaat gaccaatcaa tttattttaaa 240  
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 cagtctttgc aatctggctt tgtctgtgat tgctcttgta tagtaggtct gtccagaaat 600  
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<210> 118
<211> 86
<212> PRT
<213> Homo sapiens

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<400> 118
Met Val Arg Lys Val Asn Ala His Leu Pro Leu Ser Phe Pro Thr Val
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Glu Thr Asp Ser Arg Glu Ile Leu Gln Val Arg Cys Tyr Val Gly Leu
      20             25             30

Arg Glu Arg Cys Tyr Asp Gln Thr Glu Pro Phe Ser Leu Pro Ser Val
      35             40             45

His Gly Phe Ser Trp Leu Cys Gly Pro Val Ser Cys His Ser Phe Thr
      50             55             60

Pro Asn Phe Trp Asp Ile Gln Gly Asn Asn Leu Ala Thr Gly Tyr Leu
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Leu Val Glu Ile Met Trp
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<210> 119
<211> 29
<212> DNA
<213> Artificial Sequence

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<220>
<223> oligonucleotide

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<220>
<221> misc_feature
<222> (2)
<223> biotinylated phosphoramidite residue

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<400> 119

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<210> 120  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<220>  
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<400> 120  
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<210> 121  
 <211> 29  
 <212> DNA  
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<220>  
 <223> oligonucleotide

<220>  
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<400> 121  
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<210> 122  
 <211> 29  
 <212> DNA  
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<220>  
 <223> oligonucleotide

<220>  
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<400> 122  
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<210> 123  
 <211> 29  
 <212> DNA  
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<220>  
 <223> oligonucleotide

<220>  
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<222> (2)  
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<400> 123  
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<210> 124  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
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<400> 124  
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29

<210> 125  
<211> 29  
<212> DNA  
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<220>  
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<220>  
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<400> 125  
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<210> 126  
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<220>  
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<400> 126  
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<210> 127  
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<210> 152

<211> 29

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29

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Arg Arg Ser Ala Met Leu Cys Ile Leu Thr Val Pro Ala Ala Met Thr  
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Ser His Asp Leu Met Lys Phe Val Ala Pro Phe Asn Glu Val Ile Glu  
35 40 45  
Gln Met Lys Ile Ile Arg Asp Ser Thr Pro Asn Gln Tyr Met Val Leu  
50 55 60  
Ile Lys Phe Arg Ala Gln Ala Asp Ala Asp Ser Phe Tyr Met Thr Cys  
65 70 75 80  
Asn Gly Arg Gln Phe Asn Ser Ile Glu Asp Asp Val Cys Gln Leu Val  
85 90 95  
Tyr Val Glu Arg Ala Glu Val Leu Lys Ser Glu Asp Gly Ala Ser Leu  
100 105 110  
Pro Val Met Asp Leu Thr Glu Leu Pro Lys Cys Thr Val Cys Leu Glu  
115 120 125  
Arg Met Asp Glu Ser Val Asn Gly Ile Leu Thr Thr Leu Cys Asn His  
130 135 140  
Ser Phe His Ser Gln Cys Leu Gln Arg Trp Asp Asp Thr Thr Cys Pro  
145 150 155 160  
Val Cys Arg Tyr Cys Gln Thr Pro Glu Pro Val Glu Glu Asn Lys Cys  
165 170 175  
Phe Glu Cys Gly Val Gln Glu Asn Leu Trp Ile Cys Leu Ile Cys Gly  
180 185 190  
His Ile Gly Cys Gly Arg Tyr Val Ser Arg His Ala Tyr Lys His Phe  
195 200 205  
Glu Glu Thr Gln His Thr Tyr Ala Met Gln Leu Thr Asn His Arg Val  
210 215 220  
Trp Asp Tyr Ala Gly Asp Asn Tyr Val His Arg Leu Val Ala Ser Lys  
225 230 235 240  
Thr Asp Gly Lys Ile Val Gln Tyr Glu Cys Glu Gly Asp Thr Cys Gln  
245 250 255  
Glu Glu Lys Ile Asp Ala Leu Gln Leu Glu Tyr Ser Tyr Leu Leu Thr  
260 265 270



Ser Gln Leu Glu Ser Gln Arg Ile Tyr Trp Glu Asn Lys Ile Val Arg  
275 280 285

Ile Glu Lys Asp Thr Ala Glu Glu Ile Asn Asn Met Lys Thr Lys Phe  
290 295 300

Lys Glu Thr Ile Glu Lys Cys Asp Asn Leu Glu His Lys Leu Asn Asp  
305 310 315 320

Leu Leu Lys Glu Lys Gln Ser Val Glu Arg Lys Cys Thr Gln Leu Asn  
325 330 335

Thr Lys Val Ala Lys Leu Thr Asn Glu Leu Lys Glu Glu Gln Glu Met  
340 345 350

Asn Lys Cys Leu Arg Ala Asn Gln Val Leu Leu Gln Asn Lys Leu Lys  
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Glu Glu Glu Arg Val Leu Lys Glu Thr Cys Asp Gln Lys Asp Leu Gln  
370 375 380

Ile Thr Glu Ile  
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<212> PRT  
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20 25 30

Ser Gly Val Leu Ser Ser Ile Gly Lys Ile Phe Lys Glu Glu Gly Leu  
35 40 45

Leu Gly Phe Phe Val Gly Leu Ile Pro His Leu Leu Gly Asp Val Val  
50 55 60

Phe Leu Trp Gly Cys Asn Leu Leu Ala His Phe Ile Asn Ala Tyr Leu  
65 70 75 80

Val Asp Asp Ser Phe Ser Gln Ala Leu Ala Ile Arg Ser Tyr Thr Lys  
85 90 95

Phe Val Met Gly Ile Ala Val Ser Met Leu Thr Tyr Pro Phe Leu Leu  
100 105 110

Val Gly Asp Leu Met Ala Val Asn Asn Cys Gly Leu Gln Ala Gly Leu  
115 120 125

Pro Pro Tyr Ser Pro Val Phe Lys Ser Trp Ile His Cys Trp Lys Tyr  
130 135 140

Leu Ser Val Gln Gly Gln Leu Phe Arg Gly Ser Ser Leu Leu Phe Arg



11

[illegible]